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(54) Title: MOLECULES FOR DISEASE DETECTION AND TREATMENT

(57) Abstract: The present invention provides purified disease detection and treatment molecule polynucleotides (mddt). Also encompassed are the polypeptides (MDDT) encoded by mddt. The invention also provides for the use of mddt, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing mddt for the expression of MDDT. The invention additionally provides for the use of isolated and purified MDDT to induce antibodies and to screen libraries of compounds and the use of anti-MDDT antibodies in diagnostic assays. Also provided are microarrays containing mddt and methods of use.



WO 01/62922 A2



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MOLECULES FOR DISEASE DETECTION AND TREATMENT

TECHNICAL FIELD

The present invention relates to molecules for disease detection and treatment and to the use of
5 these sequences in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of molecules for disease detection and treatment.

BACKGROUND OF THE INVENTION

The human genome is comprised of thousands of genes, many encoding gene products that
10 function in the maintenance and growth of the various cells and tissues in the body. Aberrant expression or mutations in these genes and their products is the cause of, or is associated with, a variety of human diseases such as cancer and other cell proliferative disorders. The identification of these genes and their products is the basis of an ever-expanding effort to find markers for early detection of diseases, and targets for their prevention and treatment.

15 For example, cancer represents a type of cell proliferative disorder that affects nearly every tissue in the body. A wide variety of molecules, either aberrantly expressed or mutated, can be the cause of, or involved with, various cancers because tissue growth involves complex and ordered patterns of cell proliferation, cell differentiation, and apoptosis. Cell proliferation must be regulated to maintain both the number of cells and their spatial organization. This regulation depends upon the
20 appropriate expression of proteins which control cell cycle progression in response to extracellular signals such as growth factors and other mitogens, and intracellular cues such as DNA damage or nutrient starvation. Molecules which directly or indirectly modulate cell cycle progression fall into several categories, including growth factors and their receptors, second messenger and signal transduction proteins, oncogene products, tumor-suppressor proteins, and mitosis-promoting factors.
25 Aberrant expression or mutations in any of these gene products can result in cell proliferative disorders such as cancer. Oncogenes are genes generally derived from normal genes that, through abnormal expression or mutation, can effect the transformation of a normal cell to a malignant one (oncogenesis). Oncoproteins, encoded by oncogenes, can affect cell proliferation in a variety of ways and include growth factors, growth factor receptors, intracellular signal transducers, nuclear transcription factors,
30 and cell-cycle control proteins. In contrast, tumor-suppressor genes are involved in inhibiting cell proliferation. Mutations which cause reduced or loss of function in tumor-suppressor genes result in aberrant cell proliferation and cancer. Thus a wide variety of genes and their products have been found that are associated with cell proliferative disorders such as cancer, but many more may exist that are yet to be discovered.

35 DNA-based arrays can provide a simple way to explore the expression of a single polymorphic

gene or a large number of genes. When the expression of a single gene is explored, DNA-based arrays are employed to detect the expression of specific gene variants. For example, a p53 tumor suppressor gene array is used to determine whether individuals are carrying mutations that predispose them to cancer. A cytochrome p450 gene array is useful to determine whether individuals have one of a number
5 of specific mutations that could result in increased drug metabolism, drug resistance or drug toxicity.

DNA-based array technology is especially relevant for the rapid screening of expression of a large number of genes. There is a growing awareness that gene expression is affected in a global fashion. A genetic predisposition, disease or therapeutic treatment may affect, directly or indirectly, the expression of a large number of genes. In some cases the interactions may be expected, such as when
10 the genes are part of the same signaling pathway. In other cases, such as when the genes participate in separate signaling pathways, the interactions may be totally unexpected. Therefore, DNA-based arrays can be used to investigate how genetic predisposition, disease, or therapeutic treatment affects the expression of a large number of genes.

The discovery of new molecules for disease detection and treatment satisfies a need in the art
15 by providing new compositions which are useful in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of molecules for disease detection and treatment.

SUMMARY OF THE INVENTION

20 The present invention relates to human disease detection and treatment molecule polynucleotides (*mddt*) as presented in the Sequence Listing. The *mddt* uniquely identify genes encoding structural, functional, and regulatory disease detection and treatment molecules.

The invention provides an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of
25 SEQ ID NO:1-45; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). In one alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45. In another alternative,
30 the polynucleotide comprises at least 60 contiguous nucleotides of a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; c) a polynucleotide sequence complementary to a); d) a

polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The invention further provides a composition for the detection of expression of disease detection and treatment molecule polynucleotides comprising at least one isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected
5 from the group consisting of SEQ ID NO:1-45; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d); and a detectable label.

The invention also provides a method for detecting a target polynucleotide in a sample, said
10 target polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; c) a polynucleotide sequence complementary to
15 a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The method comprises a) amplifying said target polynucleotide or a fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention also provides a method for detecting a target polynucleotide in a sample, said
20 target polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; c) a polynucleotide sequence complementary to
25 a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides
30 comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof. In one alternative, the probe comprises at least 30 contiguous nucleotides. In another alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a recombinant polynucleotide comprising a promoter sequence operably linked to an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a

polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism
5 comprising the recombinant polynucleotide. In a further alternative, the invention provides a method for producing a disease detection and treatment molecule polypeptide, the method comprising a) culturing a cell under conditions suitable for expression of the disease detection and treatment molecule polypeptide, wherein said cell is transformed with the recombinant polynucleotide, and b) recovering the disease detection and treatment molecule polypeptide so expressed.

10 The invention also provides a purified disease detection and treatment molecule polypeptide (MDDT) encoded by at least one polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45. Additionally, the invention provides an isolated antibody which specifically binds to the disease detection and treatment molecule polypeptide. The invention further provides a method of identifying a test compound which specifically binds to the disease
15 detection and treatment molecule polypeptide, the method comprising the steps of a) providing a test compound; b) combining the disease detection and treatment molecule polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and c) detecting binding of the disease detection and treatment molecule polypeptide to the test compound, thereby identifying the test compound which specifically binds the disease detection and treatment molecule polypeptide.

20 The invention further provides a microarray wherein at least one element of the microarray is an isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ
25 ID NO:1-45; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The invention also provides a method for generating a transcript image of a sample which contains polynucleotides. The method comprises a) labeling the polynucleotides of the sample, b) contacting the elements of the microarray with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex,
30 and c) quantifying the expression of the polynucleotides in the sample.

Additionally, the invention provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; b) a naturally occurring polynucleotide sequence having

at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The method comprises a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide, and c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of i) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; ii) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence selected from the group consisting of i) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; ii) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45; iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv), and alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

The invention further provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:46-90, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:46-90, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:46-90, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:46-90. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:46-90.

DESCRIPTION OF THE TABLES

Table 1 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with their
5 GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 2 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with
1.0 polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments and the Pfam hits, Pfam descriptions, and E-values corresponding to the polypeptide domains encoded by the polynucleotide segments are indicated.

Table 3 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with
1.5 polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments are shown, and the polypeptides encoded by the polynucleotide segments constitute either signal peptide (SP) or transmembrane (TM) domains, as indicated. The membrane topology of the encoded polypeptide sequence is indicated, the N-terminus (N) listed as being oriented to either the cytosolic (in) or non-
2.0 cytosolic (out) side of the cell membrane or organelle.

Table 4 shows the sequence identification numbers (SEQ ID NO:s) corresponding to the polynucleotides of the present invention, along with component sequence identification numbers (component IDs) corresponding to each template. The component sequences, which were used to assemble the template sequences, are defined by the indicated "start" and "stop" nucleotide positions
2.5 along each template.

Table 5 shows the tissue distribution profiles for the templates of the invention.

Table 6 shows the sequence identification numbers (SEQ ID NO:s) corresponding to the polypeptides of the present invention, along with the reading frames used to obtain the polypeptide segments, the lengths of the polypeptide segments, the "start" and "stop" nucleotide positions of the
3.0 polynucleotide sequences used to define the encoded polypeptide segments, the GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 7 summarizes the bioinformatics tools which are useful for analysis of the polynucleotides of the present invention. The first column of Table 7 lists analytical tools, programs, and algorithms, the second column provides brief descriptions thereof, the third column presents

appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences).

5

DETAILED DESCRIPTION OF THE INVENTION

Before the nucleic acid sequences and methods are presented, it is to be understood that this invention is not limited to the particular machines, methods, and materials described. Although particular embodiments are described, machines, methods, and materials similar or equivalent to these
10 embodiments may be used to practice the invention. The preferred machines, methods, and materials set forth are not intended to limit the scope of the invention which is limited only by the appended claims.

The singular forms “a”, “an”, and “the” include plural reference unless the context clearly dictates otherwise. All technical and scientific terms have the meanings commonly understood by one
15 of ordinary skill in the art. All publications are incorporated by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are presented and which might be used in connection with the invention. Nothing in the specification is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

Definitions

As used herein, the lower case “mddt” refers to a nucleic acid sequence, while the upper case “MDDT” refers to an amino acid sequence encoded by mddt. A “full-length” mddt refers to a nucleic acid sequence containing the entire coding region of a gene endogenously expressed in human tissue.

“Adjuvants” are materials such as Freund's adjuvant, mineral gels (aluminum hydroxide), and
25 surface active substances (lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol) which may be administered to increase a host's immunological response.

“Allele” refers to an alternative form of a nucleic acid sequence. Alleles result from a
“mutation,” a change or an alternative reading of the genetic code. Any given gene may have none, one,
30 or many allelic forms. Mutations which give rise to alleles include deletions, additions, or substitutions of nucleotides. Each of these changes may occur alone, or in combination with the others, one or more times in a given nucleic acid sequence. The present invention encompasses allelic mddt.

“Amino acid sequence” refers to a peptide, a polypeptide, or a protein of either natural or synthetic origin. The amino acid sequence is not limited to the complete, endogenous amino acid

sequence and may be a fragment, epitope, variant, or derivative of a protein expressed by a nucleic acid sequence.

“Amplification” refers to the production of additional copies of a sequence and is carried out using polymerase chain reaction (PCR) technologies well known in the art.

5 “Antibody” refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind MDDT polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and
10 can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

“Antisense sequence” refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence may include DNA, RNA, or any nucleic acid mimic or analog such
15 as peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine.

“Antisense sequence” refers to a sequence capable of specifically hybridizing to a target
20 sequence. The antisense sequence can be DNA, RNA, or any nucleic acid mimic or analog.

“Antisense technology” refers to any technology which relies on the specific hybridization of an antisense sequence to a target sequence.

A “bin” is a portion of computer memory space used by a computer program for storage of data, and bounded in such a manner that data stored in a bin may be retrieved by the program.

25 “Biologically active” refers to an amino acid sequence having a structural, regulatory, or biochemical function of a naturally occurring amino acid sequence.

“Clone joining” is a process for combining gene bins based upon the bins' containing sequence information from the same clone. The sequences may assemble into a primary gene transcript as well as one or more splice variants.

30 “Complementary” describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing (5'-A-G-T-3' pairs with its complement 3'-T-C-A-5').

A “component sequence” is a nucleic acid sequence selected by a computer program such as PHRED and used to assemble a consensus or template sequence from one or more component sequences.

A "consensus sequence" or "template sequence" is a nucleic acid sequence which has been assembled from overlapping sequences, using a computer program for fragment assembly such as the GELVIEW fragment assembly system (Genetics Computer Group (GCG), Madison WI) or using a relational database management system (RDMS).

5 "Conservative amino acid substitutions" are those substitutions that, when made, least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

10

	Original Residue	Conservative Substitution
	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
15	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
20	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
25	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
30	Val	Ile, Leu, Thr

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or
 35 hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

"Deletion" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or amino acid residue, respectively, is absent.

"Derivative" refers to the chemical modification of a nucleic acid sequence, such as by replacement of hydrogen by an alkyl, acyl, amino, hydroxyl, or other group.

40 The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

"E-value" refers to the statistical probability that a match between two sequences occurred by chance.

A "fragment" is a unique portion of mddt or MDDT which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 10 to 1000 contiguous amino acid residues or nucleotides. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous amino acid residues or nucleotides in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing and the figures, may be encompassed by the present embodiments.

A fragment of mddt comprises a region of unique polynucleotide sequence that specifically identifies mddt, for example, as distinct from any other sequence in the same genome. A fragment of mddt is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish mddt from related polynucleotide sequences. The precise length of a fragment of mddt and the region of mddt to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of MDDT is encoded by a fragment of mddt. A fragment of MDDT comprises a region of unique amino acid sequence that specifically identifies MDDT. For example, a fragment of MDDT is useful as an immunogenic peptide for the development of antibodies that specifically recognize MDDT. The precise length of a fragment of MDDT and the region of MDDT to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" nucleotide sequence is one containing at least a start site for translation to a protein sequence, followed by an open reading frame and a stop site, and encoding a "full length" polypeptide.

"Hit" refers to a sequence whose annotation will be used to describe a given template. Criteria for selecting the top hit are as follows: if the template has one or more exact nucleic acid matches, the top hit is the exact match with highest percent identity. If the template has no exact matches but has significant protein hits, the top hit is the protein hit with the lowest E-value. If the template has no significant protein hits, but does have significant non-exact nucleotide hits, the top hit is the nucleotide hit with the lowest E-value.

“Homology” refers to sequence similarity either between a reference nucleic acid sequence and at least a fragment of an mddt or between a reference amino acid sequence and a fragment of an MDDT.

“Hybridization” refers to the process by which a strand of nucleotides anneals with a complementary strand through base pairing. Specific hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific hybridization complexes form under defined annealing conditions, and remain hybridized after the “washing” step. The defined hybridization conditions include the annealing conditions and the washing step(s), the latter of which is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid probes that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency.

Generally, stringency of hybridization is expressed with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization is well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, or 55°C may be used. SSC concentration may be varied from about 0.2 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 µg/ml. Useful variations on these conditions will be readily apparent to those skilled in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their resultant proteins.

Other parameters, such as temperature, salt concentration, and detergent concentration may be varied to achieve the desired stringency. Denaturants, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as RNA:DNA hybridizations. Appropriate hybridization conditions are routinely determinable by one of ordinary skill in the art.

“Immunogenic” describes the potential for a natural, recombinant, or synthetic peptide, epitope, polypeptide, or protein to induce antibody production in appropriate animals, cells, or cell lines.

“Insertion” or “addition” refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or residue, respectively, is added to the sequence.

5 “Labeling” refers to the covalent or noncovalent joining of a polynucleotide, polypeptide, or antibody with a reporter molecule capable of producing a detectable or measurable signal.

“Microarray” is any arrangement of nucleic acids, amino acids, antibodies, etc., on a substrate. The substrate may be a solid support such as beads, glass, paper, nitrocellulose, nylon, or an appropriate membrane.

10 “Linkers” are short stretches of nucleotide sequence which may be added to a vector or an mddt to create restriction endonuclease sites to facilitate cloning. “Polylinkers” are engineered to incorporate multiple restriction enzyme sites and to provide for the use of enzymes which leave 5' or 3' overhangs (e.g., BamHI, EcoRI, and HindIII) and those which provide blunt ends (e.g., EcoRV, SnaBI, and StuI).

“Naturally occurring” refers to an endogenous polynucleotide or polypeptide that may be
15 isolated from viruses or prokaryotic or eukaryotic cells.

“Nucleic acid sequence” refers to the specific order of nucleotides joined by phosphodiester bonds in a linear, polymeric arrangement. Depending on the number of nucleotides, the nucleic acid sequence can be considered an oligomer, oligonucleotide, or polynucleotide. The nucleic acid can be DNA, RNA, or any nucleic acid analog, such as PNA, may be of genomic or synthetic origin, may be
20 either double-stranded or single-stranded, and can represent either the sense or antisense (complementary) strand.

“Oligomer” refers to a nucleic acid sequence of at least about 6 nucleotides and as many as about 60 nucleotides, preferably about 15 to 40 nucleotides, and most preferably between about 20 and 30 nucleotides, that may be used in hybridization or amplification technologies. Oligomers may be used
25 as, e.g., primers for PCR, and are usually chemically synthesized.

“Operably linked” refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and,
30 where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to a DNA mimic in which nucleotide bases are attached to a pseudopeptide backbone to increase stability. PNAs, also designated antigene agents, can prevent gene expression by targeting complementary messenger RNA.

The phrases “percent identity” and “% identity”, as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore
5 achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G.
10 and Sharp, P.M. (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and “diagonals saved”=4. The “weighted” residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polynucleotide sequence pairs.

15 Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis
20 programs including “blastn,” that is used to determine alignment between a known polynucleotide sequence and other sequences on a variety of databases. Also available is a tool called “BLAST 2 Sequences” that is used for direct pairwise comparison of two nucleotide sequences. “BLAST 2 Sequences” can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2/>. The “BLAST 2 Sequences” tool can be used for both blastn and blastp (discussed below). BLAST
25 programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the “BLAST 2 Sequences” tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

30 *Penalty for mismatch: -2*

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases “percent identity” and “% identity”, as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the hydrophobicity and acidity of the substituted residue, thus preserving the structure (and therefore function) of the folded polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and “diagonals saved”=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the “BLAST 2 Sequences” tool Version 2.0.9 (May-07-1999) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalty

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150
5 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

“Post-translational modification” of an MDDT may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the
10 art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu and the MDDT.

“Probe” refers to mddt or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent
15 agents, and enzymes. “Primers” are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous
20 nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the figures and Sequence Listing, may be used.

25 Methods for preparing and using probes and primers are described in the references, for example Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel et al., 1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from
30 a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000

nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

"Purified" refers to molecules, either polynucleotides or polypeptides that are isolated or separated from their natural environment and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other compounds with which they are naturally associated.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

"Regulatory element" refers to a nucleic acid sequence from nontranslated regions of a gene,

and includes enhancers, promoters, introns, and 3' untranslated regions, which interact with host proteins to carry out or regulate transcription or translation.

“Reporter” molecules are chemical or biochemical moieties used for labeling a nucleic acid, an amino acid, or an antibody. They include radionuclides; enzymes; fluorescent, chemiluminescent, or
5 chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An “RNA equivalent,” in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose
10 instead of deoxyribose.

“Sample” is used in its broadest sense. Samples may contain nucleic or amino acids, antibodies, or other materials, and may be derived from any source (e.g., bodily fluids including, but not limited to, saliva, blood, and urine; chromosome(s), organelles, or membranes isolated from a cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; and cleared cells or tissues or blots
15 or imprints from such cells or tissues).

“Specific binding” or “specifically binding” refers to the interaction between a protein or peptide and its agonist, antibody, antagonist, or other binding partner. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope “A,” the
20 presence of a polypeptide containing epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

“Substitution” refers to the replacement of at least one nucleotide or amino acid by a different nucleotide or amino acid.

25 “Substrate” refers to any suitable rigid or semi-rigid support including, e.g., membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles or capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A “transcript image” refers to the collective pattern of gene expression by a particular tissue or
30 cell type under given conditions at a given time.

“Transformation” refers to a process by which exogenous DNA enters a recipient cell. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being

transformed.

“Transformants” include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as cells which transiently express inserted DNA or RNA.

5 A “transgenic organism,” as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant
10 virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, and plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques
15 for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A “variant” of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 25% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the “BLAST 2 Sequences” tool Version 2.0.9 (May-07-1999)
20 set at default parameters. Such a pair of nucleic acids may show, for example, at least 30%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or even at least 98% or greater sequence identity over a certain defined length. The variant may result in “conservative” amino acid changes which do not affect structural and/or chemical properties. A variant may be described as, for example, an “allelic” (as defined above), “splice,” “species,” or “polymorphic” variant. A splice
25 variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant
30 amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass “single nucleotide polymorphisms” (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

In an alternative, variants of the polynucleotides of the present invention may be generated through recombinant methods. One possible method is a DNA shuffling technique such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of MDDT, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 98% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

In a particular embodiment, cDNA sequences derived from human tissues and cell lines were aligned based on nucleotide sequence identity and assembled into "consensus" or "template" sequences which are designated by the template identification numbers (template IDs) in column 2 of Table 1. The sequence identification numbers (SEQ ID NO:s) corresponding to the template IDs are shown in column 1. The template sequences have similarity to GenBank sequences, or "hits," as designated by the GI Numbers in column 3. The statistical probability of each GenBank hit is indicated by a probability score in column 4, and the functional annotation corresponding to each GenBank hit is listed in column 5.

The invention incorporates the nucleic acid sequences of these templates as disclosed in the Sequence Listing and the use of these sequences in the diagnosis and treatment of disease states

characterized by defects in disease detection and treatment molecules. The invention further utilizes these sequences in hybridization and amplification technologies, and in particular, in technologies which assess gene expression patterns correlated with specific cells or tissues and their responses in vivo or in vitro to pharmaceutical agents, toxins, and other treatments. In this manner, the sequences of the present invention are used to develop a transcript image for a particular cell or tissue.

Derivation of Nucleic Acid Sequences

cDNA was isolated from libraries constructed using RNA derived from normal and diseased human tissues and cell lines. The human tissues and cell lines used for cDNA library construction were selected from a broad range of sources to provide a diverse population of cDNAs representative of gene transcription throughout the human body. Descriptions of the human tissues and cell lines used for cDNA library construction are provided in the LIFESEQ database (Incyte Genomics, Inc. (Incyte), Palo Alto CA). Human tissues were broadly selected from, for example, cardiovascular, dermatologic, endocrine, gastrointestinal, hematopoietic/immune system, musculoskeletal, neural, reproductive, and urologic sources.

Cell lines used for cDNA library construction were derived from, for example, leukemic cells, teratocarcinomas, neuroepitheliomas, cervical carcinoma, lung fibroblasts, and endothelial cells. Such cell lines include, for example, THP-1, Jurkat, HUVEC, hNT2, WI38, HeLa, and other cell lines commonly used and available from public depositories (American Type Culture Collection, Manassas VA). Prior to mRNA isolation, cell lines were untreated, treated with a pharmaceutical agent such as 5'-aza-2'-deoxycytidine, treated with an activating agent such as lipopolysaccharide in the case of leukocytic cell lines, or, in the case of endothelial cell lines, subjected to shear stress.

Sequencing of the cDNAs

Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ the Klenow fragment of DNA polymerase I, SEQUENASE DNA polymerase (U.S. Biochemical Corporation, Cleveland OH), Taq polymerase (Applied Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Inc. (Amersham Pharmacia Biotech), Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies Inc. (Life Technologies), Gaithersburg MD), to extend the nucleic acid sequence from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. Chain termination reaction products may be electrophoresed on urea-polyacrylamide gels and detected either by autoradiography (for radioisotope-labeled nucleotides) or by fluorescence (for

fluorophore-labeled nucleotides). Automated methods for mechanized reaction preparation, sequencing, and analysis using fluorescence detection methods have been developed. Machines used to prepare cDNAs for sequencing can include the MICROLAB 2200 liquid transfer system (Hamilton Company (Hamilton), Reno NV), Peltier thermal cycler (PTC200; MJ Research, Inc. (MJ Research), Watertown MA), and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing can be carried out using, for example, the ABI 373 or 377 (Applied Biosystems) or MEGABACE 1000 (Molecular Dynamics, Inc. (Molecular Dynamics), Sunnyvale CA) DNA sequencing systems, or other automated and manual sequencing systems well known in the art.

The nucleotide sequences of the Sequence Listing have been prepared by current, state-of-the-art, automated methods and, as such, may contain occasional sequencing errors or unidentified nucleotides. Such unidentified nucleotides are designated by an N. These infrequent unidentified bases do not represent a hindrance to practicing the invention for those skilled in the art. Several methods employing standard recombinant techniques may be used to correct errors and complete the missing sequence information. (See, e.g., those described in Ausubel, F.M. et al. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY; and Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY.)

Assembly of cDNA Sequences

Human polynucleotide sequences may be assembled using programs or algorithms well known in the art. Sequences to be assembled are related, wholly or in part, and may be derived from a single or many different transcripts. Assembly of the sequences can be performed using such programs as PHRAP (Phils Revised Assembly Program) and the GELVIEW fragment assembly system (GCG), or other methods known in the art.

Alternatively, cDNA sequences are used as “component” sequences that are assembled into “template” or “consensus” sequences as follows. Sequence chromatograms are processed, verified, and quality scores are obtained using PHRED. Raw sequences are edited using an editing pathway known as Block 1 (See, e.g., the LIFESEQ Assembled User Guide, Incyte Genomics, Palo Alto, CA). A series of BLAST comparisons is performed and low-information segments and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) are replaced by “n’s”, or masked, to prevent spurious matches. Mitochondrial and ribosomal RNA sequences are also removed. The processed sequences are then loaded into a relational database management system (RDMS) which assigns edited sequences to existing templates, if available. When additional sequences are added into the RDMS, a process is initiated which modifies existing templates or creates new templates from works in

progress (i.e., nonfinal assembled sequences) containing queued sequences or the sequences themselves. After the new sequences have been assigned to templates, the templates can be merged into bins. If multiple templates exist in one bin, the bin can be split and the templates reannotated.

Once gene bins have been generated based upon sequence alignments, bins are "clone joined" based upon clone information. Clone joining occurs when the 5' sequence of one clone is present in one bin and the 3' sequence from the same clone is present in a different bin, indicating that the two bins should be merged into a single bin. Only bins which share at least two different clones are merged.

A resultant template sequence may contain either a partial or a full length open reading frame, or all or part of a genetic regulatory element. This variation is due in part to the fact that the full length cDNAs of many genes are several hundred, and sometimes several thousand, bases in length. With current technology, cDNAs comprising the coding regions of large genes cannot be cloned because of vector limitations, incomplete reverse transcription of the mRNA, or incomplete "second strand" synthesis. Template sequences may be extended to include additional contiguous sequences derived from the parent RNA transcript using a variety of methods known to those of skill in the art. Extension may thus be used to achieve the full length coding sequence of a gene.

Analysis of the cDNA Sequences

The cDNA sequences are analyzed using a variety of programs and algorithms which are well known in the art. (See, e.g., Ausubel, 1997, supra, Chapter 7.7; Meyers, R.A. (Ed.) (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853; and Table 7.) These analyses comprise both reading frame determinations, e.g., based on triplet codon periodicity for particular organisms (Fickett, J.W. (1982) Nucleic Acids Res. 10:5303-5318); analyses of potential start and stop codons; and homology searches.

Computer programs known to those of skill in the art for performing computer-assisted searches for amino acid and nucleic acid sequence similarity, include, for example, Basic Local Alignment Search Tool (BLAST; Altschul, S.F. (1993) J. Mol. Evol. 36:290-300; Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410). BLAST is especially useful in determining exact matches and comparing two sequence fragments of arbitrary but equal lengths, whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user (Karlin, S. et al. (1988) Proc. Natl. Acad. Sci. USA 85:841-845). Using an appropriate search tool (e.g., BLAST or HMM), GenBank, SwissProt, BLOCKS, PFAM and other databases may be searched for sequences containing regions of homology to a query mddt or MDDT of the present invention.

Other approaches to the identification, assembly, storage, and display of nucleotide and polypeptide sequences are provided in "Relational Database for Storing Biomolecule Information,"

U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S.S.N. 08/811,758, filed March 6, 1997; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein in their entirety.

5 Protein hierarchies can be assigned to the putative encoded polypeptide based on, e.g., motif, BLAST, or biological analysis. Methods for assigning these hierarchies are described, for example, in "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S.S.N. 08/812,290, filed March 6, 1997, incorporated herein by reference.

10 Human Disease Detection and Treatment Molecule Sequences

The mddt of the present invention may be used for a variety of diagnostic and therapeutic purposes. For example, an mddt may be used to diagnose a particular condition, disease, or disorder associated with disease detection and treatment molecules. Such conditions, diseases, and disorders include, but are not limited to, a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and an autoimmune/inflammatory disorder, such as actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma. The mddt can be used to detect the presence of,

35

or to quantify the amount of, an mddt-related polynucleotide in a sample. This information is then compared to information obtained from appropriate reference samples, and a diagnosis is established. Alternatively, a polynucleotide complementary to a given mddt can inhibit or inactivate a therapeutically relevant gene related to the mddt.

5

Analysis of mddt Expression Patterns

The expression of mddt may be routinely assessed by hybridization-based methods to determine, for example, the tissue-specificity, disease-specificity, or developmental stage-specificity of mddt expression. For example, the level of expression of mddt may be compared among different cell types or tissues, among diseased and normal cell types or tissues, among cell types or tissues at different developmental stages, or among cell types or tissues undergoing various treatments. This type of analysis is useful, for example, to assess the relative levels of mddt expression in fully or partially differentiated cells or tissues, to determine if changes in mddt expression levels are correlated with the development or progression of specific disease states, and to assess the response of a cell or tissue to a specific therapy, for example, in pharmacological or toxicological studies. Methods for the analysis of mddt expression are based on hybridization and amplification technologies and include membrane-based procedures such as northern blot analysis, high-throughput procedures that utilize, for example, microarrays, and PCR-based procedures.

20 Hybridization and Genetic Analysis

The mddt, their fragments, or complementary sequences, may be used to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid sequences. The mddt may be hybridized to naturally occurring or recombinant nucleic acid sequences under appropriately selected temperatures and salt concentrations. Hybridization with a probe based on the nucleic acid sequence of at least one of the mddt allows for the detection of nucleic acid sequences, including genomic sequences, which are identical or related to the mddt of the Sequence Listing. Probes may be selected from non-conserved or unique regions of at least one of the polynucleotides of SEQ ID NO:1-45 and tested for their ability to identify or amplify the target nucleic acid sequence using standard protocols.

30 Polynucleotide sequences that are capable of hybridizing, in particular, to those shown in SEQ ID NO:1-45 and fragments thereof, can be identified using various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions are discussed in "Definitions."

A probe for use in Southern or northern hybridization may be derived from a fragment of an

mddt sequence, or its complement, that is up to several hundred nucleotides in length and is either single-stranded or double-stranded. Such probes may be hybridized in solution to biological materials such as plasmids, bacterial, yeast, or human artificial chromosomes, cleared or sectioned tissues, or to artificial substrates containing mddt. Microarrays are particularly suitable for identifying the presence of and detecting the level of expression for multiple genes of interest by examining gene expression correlated with, e.g., various stages of development, treatment with a drug or compound, or disease progression. An array analogous to a dot or slot blot may be used to arrange and link polynucleotides to the surface of a substrate using one or more of the following: mechanical (vacuum), chemical, thermal, or UV bonding procedures. Such an array may contain any number of mddt and may be produced by hand or by using available devices, materials, and machines.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

Probes may be labeled by either PCR or enzymatic techniques using a variety of commercially available reporter molecules. For example, commercial kits are available for radioactive and chemiluminescent labeling (Amersham Pharmacia Biotech) and for alkaline phosphatase labeling (Life Technologies). Alternatively, mddt may be cloned into commercially available vectors for the production of RNA probes. Such probes may be transcribed in the presence of at least one labeled nucleotide (e.g., ³²P-ATP, Amersham Pharmacia Biotech).

Additionally the polynucleotides of SEQ ID NO:1-45 or suitable fragments thereof can be used to isolate full length cDNA sequences utilizing hybridization and/or amplification procedures well known in the art, e.g., cDNA library screening, PCR amplification, etc. The molecular cloning of such full length cDNA sequences may employ the method of cDNA library screening with probes using the hybridization, stringency, washing, and probing strategies described above and in Ausubel, *supra*, Chapters 3, 5, and 6. These procedures may also be employed with genomic libraries to isolate genomic sequences of mddt in order to analyze, e.g., regulatory elements.

Genetic Mapping

Gene identification and mapping are important in the investigation and treatment of almost all conditions, diseases, and disorders. Cancer, cardiovascular disease, Alzheimer's disease, arthritis, diabetes, and mental illnesses are of particular interest. Each of these conditions is more complex than the single gene defects of sickle cell anemia or cystic fibrosis, with select groups of genes being

predictive of predisposition for a particular condition, disease, or disorder. For example, cardiovascular disease may result from malfunctioning receptor molecules that fail to clear cholesterol from the bloodstream, and diabetes may result when a particular individual's immune system is activated by an infection and attacks the insulin-producing cells of the pancreas. In some studies, 5 Alzheimer's disease has been linked to a gene on chromosome 21; other studies predict a different gene and location. Mapping of disease genes is a complex and reiterative process and generally proceeds from genetic linkage analysis to physical mapping.

As a condition is noted among members of a family, a genetic linkage map traces parts of chromosomes that are inherited in the same pattern as the condition. Statistics link the inheritance of 10 particular conditions to particular regions of chromosomes, as defined by RFLP or other markers. (See, for example, Lander, E. S. and Botstein, D. (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.) Occasionally, genetic markers and their locations are known from previous studies. More often, however, the markers are simply stretches of DNA that differ among individuals. Examples of genetic linkage maps can be found in various scientific journals or at the Online Mendelian Inheritance in Man 15 (OMIM) World Wide Web site.

In another embodiment of the invention, mddt sequences may be used to generate hybridization probes useful in chromosomal mapping of naturally occurring genomic sequences. Either coding or noncoding sequences of mddt may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of an mddt coding sequence among 20 members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. 25 Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Meyers, supra, pp. 965-968.) Correlation 30 between the location of mddt on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The mddt sequences may also be used to detect polymorphisms that are genetically linked to the inheritance of a particular condition, disease, or disorder.

In situ hybridization of chromosomal preparations and genetic mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending existing genetic

maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of the corresponding human chromosome is not known. These new marker sequences can be mapped to human chromosomes and may provide valuable information to investigators searching for disease genes using positional cloning
5 or other gene discovery techniques. Once a disease or syndrome has been crudely correlated by genetic linkage with a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequences of the subject invention may also be used to detect differences in chromosomal architecture due to translocation, inversion, etc.,
10 among normal, carrier, or affected individuals.

Once a disease-associated gene is mapped to a chromosomal region, the gene must be cloned in order to identify mutations or other alterations (e.g., translocations or inversions) that may be correlated with disease. This process requires a physical map of the chromosomal region containing the disease-gene of interest along with associated markers. A physical map is necessary for determining the
15 nucleotide sequence of and order of marker genes on a particular chromosomal region. Physical mapping techniques are well known in the art and require the generation of overlapping sets of cloned DNA fragments from a particular organelle, chromosome, or genome. These clones are analyzed to reconstruct and catalog their order. Once the position of a marker is determined, the DNA from that region is obtained by consulting the catalog and selecting clones from that region. The gene of interest
20 is located through positional cloning techniques using hybridization or similar methods.

Diagnostic Uses

The mddt of the present invention may be used to design probes useful in diagnostic assays. Such assays, well known to those skilled in the art, may be used to detect or confirm conditions,
25 disorders, or diseases associated with abnormal levels of mddt expression. Labeled probes developed from mddt sequences are added to a sample under hybridizing conditions of desired stringency. In some instances, mddt, or fragments or oligonucleotides derived from mddt, may be used as primers in amplification steps prior to hybridization. The amount of hybridization complex formed is quantified and compared with standards for that cell or tissue. If mddt expression varies significantly from the
30 standard, the assay indicates the presence of the condition, disorder, or disease. Qualitative or quantitative diagnostic methods may include northern, dot blot, or other membrane or dip-stick based technologies or multiple-sample format technologies such as PCR, enzyme-linked immunosorbent assay (ELISA)-like, pin, or chip-based assays.

The probes described above may also be used to monitor the progress of conditions, disorders, or diseases associated with abnormal levels of mddt expression, or to evaluate the efficacy of a particular therapeutic treatment. The candidate probe may be identified from the mddt that are specific to a given human tissue and have not been observed in GenBank or other genome databases. Such a
5 probe may be used in animal studies, preclinical tests, clinical trials, or in monitoring the treatment of an individual patient. In a typical process, standard expression is established by methods well known in the art for use as a basis of comparison, samples from patients affected by the disorder or disease are combined with the probe to evaluate any deviation from the standard profile, and a therapeutic agent is administered and effects are monitored to generate a treatment profile. Efficacy
10 is evaluated by determining whether the expression progresses toward or returns to the standard normal pattern. Treatment profiles may be generated over a period of several days or several months. Statistical methods well known to those skilled in the art may be used to determine the significance of such therapeutic agents.

The polynucleotides are also useful for identifying individuals from minute biological samples,
15 for example, by matching the RFLP pattern of a sample's DNA to that of an individual's DNA. The polynucleotides of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, an individual can be identified through a unique set of DNA sequences. Once a unique ID
20 database is established for an individual, positive identification of that individual can be made from extremely small tissue samples.

In a particular aspect, oligonucleotide primers derived from the mddt of the invention may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP
25 detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from mddt are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these
30 differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequences of individual overlapping DNA fragments which assemble into a common consensus

sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

5 DNA-based identification techniques are critical in forensic technology. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using, e.g., PCR, to identify individuals. (See, e.g., Erlich, H. (1992) PCR Technology, Freeman and Co., New York, NY). Similarly, polynucleotides of the present invention can be used as polymorphic markers.

10 There is also a need for reagents capable of identifying the source of a particular tissue. Appropriate reagents can comprise, for example, DNA probes or primers prepared from the sequences of the present invention that are specific for particular tissues. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

15 The polynucleotides of the present invention can also be used as molecular weight markers on nucleic acid gels or Southern blots, as diagnostic probes for the presence of a specific mRNA in a particular cell type, in the creation of subtracted cDNA libraries which aid in the discovery of novel polynucleotides, in selection and synthesis of oligomers for attachment to an array or other support, and as an antigen to elicit an immune response.

20 Disease Model Systems Using mddt

The mddt of the invention or their mammalian homologs may be “knocked out” in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as
25 the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (*neo*; Capecchi, M.R. (1989) *Science* 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of
30 interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) *Clin. Invest.* 97:1999-2002; Wagner, K.U. et al. (1997) *Nucleic Acids Res.* 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus

generated may be tested with potential therapeutic or toxic agents.

The mddt of the invention may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

The mddt of the invention can also be used to create “knockin” humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of mddt is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress mddt, resulting, e.g., in the secretion of MDDT in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

15

Screening Assays

MDDT encoded by polynucleotides of the present invention may be used to screen for molecules that bind to or are bound by the encoded polypeptides. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the bound molecule. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a ligand or fragment thereof, a natural substrate, or a structural or functional mimetic. (See, Coligan et al., (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or to at least a fragment of the receptor, e.g., the active site. In either case, the molecule can be rationally designed using known techniques. Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing the polypeptide or cell membrane fractions which contain the expressed polypeptide are then contacted with a test compound and binding, stimulation, or inhibition of activity of either the polypeptide or the molecule is analyzed.

30

An assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. Alternatively, the assay may assess binding in the presence of a labeled competitor.

Additionally, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay using, e.g., a monoclonal or polyclonal antibody, can measure polypeptide level in a sample. The antibody can measure polypeptide level by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of the above assays can be used in a diagnostic or prognostic context. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

15 Transcript Imaging and Toxicological Testing

Another embodiment relates to the use of mddt to develop a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity pertaining to disease detection and treatment molecules.

Transcript images which profile mddt expression may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect mddt expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile mddt expression may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are

indicative of mechanisms of action and toxicity (Nuwaysir, E. F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and Anderson, N. L. (2000) Toxicol. Lett. 112-113:467-71, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of MDDT encoded by polynucleotides of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is

generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for
5 example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for MDDT to quantify the
10 levels of MDDT expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-11; Mendozze, L. G. et al. (1999) *Biotechniques* 27:778-88). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-
15 reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N. L. and Seilhamer, J. (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the
20 analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological
25 sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the MDDT encoded by polynucleotides of
30 the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the MDDT encoded by polynucleotides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological

sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Transcript images may be used to profile mddt expression in distinct tissue types. This process
5 can be used to determine disease detection and treatment molecule activity in a particular tissue type relative to this activity in a different tissue type. Transcript images may be used to generate a profile of mddt expression characteristic of diseased tissue. Transcript images of tissues before and after treatment may be used for diagnostic purposes, to monitor the progression of disease, and to monitor the efficacy of drug treatments for diseases which affect the activity of disease detection and treatment
10 molecules.

Transcript images of cell lines can be used to assess disease detection and treatment molecule activity and/or to identify cell lines that lack or misregulate this activity. Such cell lines may then be treated with pharmaceutical agents, and a transcript image following treatment may indicate the efficacy of these agents in restoring desired levels of this activity. A similar approach may be used to
15 assess the toxicity of pharmaceutical agents as reflected by undesirable changes in disease detection and treatment molecule activity. Candidate pharmaceutical agents may be evaluated by comparing their associated transcript images with those of pharmaceutical agents of known effectiveness.

Antisense Molecules

20 The polynucleotides of the present invention are useful in antisense technology. Antisense technology or therapy relies on the modulation of expression of a target protein through the specific binding of an antisense sequence to a target sequence encoding the target protein or directing its expression. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ; Alama, A. et al. (1997) *Pharmacol. Res.* 36(3):171-178; Crooke, S.T. (1997) *Adv. Pharmacol.*
25 40:1-49; Sharma, H.W. and R. Narayanan (1995) *Bioessays* 17(12):1055-1063; and Lavrosky, Y. et al. (1997) *Biochem. Mol. Med.* 62(1):11-22.) An antisense sequence is a polynucleotide sequence capable of specifically hybridizing to at least a portion of the target sequence. Antisense sequences bind to cellular mRNA and/or genomic DNA, affecting translation and/or transcription. Antisense sequences can be DNA, RNA, or nucleic acid mimics and analogs. (See, e.g., Rossi, J.J. et al. (1991)
30 *Antisense Res. Dev.* 1(3):285-288; Lee, R. et al. (1998) *Biochemistry* 37(3):900-1010; Pardridge, W.M. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92(12):5592-5596; and Nielsen, P. E. and Haaima, G. (1997) *Chem. Soc. Rev.* 96:73-78.) Typically, the binding which results in modulation of expression occurs through hybridization or binding of complementary base pairs. Antisense sequences can also bind to DNA duplexes through specific interactions in the major groove of the double helix.

The polynucleotides of the present invention and fragments thereof can be used as antisense sequences to modify the expression of the polypeptide encoded by mddt. The antisense sequences can be produced ex vivo, such as by using any of the ABI nucleic acid synthesizer series (Applied Biosystems) or other automated systems known in the art. Antisense sequences can also be produced
5 biologically, such as by transforming an appropriate host cell with an expression vector containing the sequence of interest. (See, e.g., Agrawal, supra.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at
10 least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E., et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J., et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY; Uckert,
15 W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

20 Expression

In order to express a biologically active MDDT, the nucleotide sequences encoding MDDT or fragments thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. Methods which are well known to those skilled in the art may be used to construct
25 expression vectors containing sequences encoding MDDT and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra, Chapters 4, 8, 16, and 17; and Ausubel, supra, Chapters 9, 10, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences
30 encoding MDDT. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or

animal (mammalian) cell systems. (See, e.g., Sambrook, *supra*; Ausubel, 1995, *supra*, Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184; Engelhard, E.K. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:3224-3227; Sandig, V. et al. (1996) *Hum. Gene Ther.* 7:1937-1945;

5 Takamatsu, N. (1987) *EMBO J.* 6:307-311; Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659; and Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.) Expression vectors derived from retroviruses, adenoviruses,

10 or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) *Cancer Gen. Ther.* 5(6):350-356; Yu, M. et al., (1993) *Proc. Natl. Acad. Sci. USA* 90(13):6340-6344; Buller, R.M. et al. (1985) *Nature* 317(6040):813-815; McGregor, D.P. et al. (1994) *Mol. Immunol.* 31(3):219-226; and Verma, I.M. and N. Somia (1997) *Nature* 389:239-242.) The invention is not

15 limited by the host cell employed.

For long term production of recombinant proteins in mammalian systems, stable expression of MDDT in cell lines is preferred. For example, sequences encoding MDDT can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Any number of

20 selection systems may be used to recover transformed cell lines. (See, e.g., Wigler, M. et al. (1977) *Cell* 11:223-232; Lowy, I. et al. (1980) *Cell* 22:817-823.; Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci. USA* 77:3567-3570; Colbere-Garapin, F. et al. (1981) *J. Mol. Biol.* 150:1-14; Hartman, S.C. and R.C.Mulligan (1988) *Proc. Natl. Acad. Sci. USA* 85:8047-8051; Rhodes, C.A. (1995) *Methods Mol. Biol.* 55:121-131.)

25

Therapeutic Uses of mddt

The mddt of the invention may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined immunodeficiency syndrome associated with an

30 inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor

VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and Somia, N. (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in mddt expression or regulation causes disease, the expression of mddt from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in mddt are treated by constructing mammalian expression vectors comprising mddt and introducing these vectors by mechanical means into mddt-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and Anderson, W.F. (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and Récipon, H. (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of mddt include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). The mddt of the invention may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and Bujard, H. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551; Gossen, M. et al., (1995) Science 268:1766-1769; Rossi, F.M.V. and Blau, H.M. (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding MDDT from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental

parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and Eb, A.J. (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

5 In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to mddt expression are treated by constructing a retrovirus vector consisting of (i) mddt under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation.

10 Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. U.S.A.* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and Miller, A.D. (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of

20 cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et al. (1997) *Blood* 89:2259-2267; Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al. (1998) *Proc. Natl. Acad. Sci. U.S.A.* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).

25 In the alternative, an adenovirus-based gene therapy delivery system is used to deliver mddt to cells which have one or more genetic abnormalities with respect to the expression of mddt. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) *Transplantation* 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) *Annu. Rev. Nutr.* 19:511-544 and Verma, I.M. and Somia, N. (1997) *Nature* 18:389:239-242, both incorporated by reference herein.

30

In another alternative, a herpes-based, gene therapy delivery system is used to deliver mddt to target cells which have one or more genetic abnormalities with respect to the expression of mddt. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing mddt to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) *Exp. Eye Res.* 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W. F. et al. 1999 *J. Virol.* 73:519-532 and Xu, H. et al., (1994) *Dev. Biol.* 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver mddt to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and Li, K-J. (1998) *Curr. Opin. Biotech.* 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting mddt into the alphavirus genome in place of the capsid-coding region results in the production of a large number of mddt RNAs and the synthesis of high levels of MDDT in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) *Virology* 228:74-83). The wide host range of alphaviruses will allow the introduction of mddt into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA

transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Antibodies

5 Anti-MDDT antibodies may be used to analyze protein expression levels. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, and Fab fragments. For descriptions of and protocols of antibody technologies, see, e.g., Pound J.D. (1998) Immunochemical Protocols, Humana Press, Totowa, NJ.

 The amino acid sequence encoded by the mddt of the Sequence Listing may be analyzed by
10 appropriate software (e.g., LASERGENE NAVIGATOR software, DNASTAR) to determine regions of high immunogenicity. The optimal sequences for immunization are selected from the C-terminus, the N-terminus, and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the polypeptide is in its natural conformation. Analysis used to select appropriate epitopes is also described by Ausubel (1997, supra, Chapter 11.7). Peptides used for
15 antibody induction do not need to have biological activity; however, they must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids, and most preferably at least 15 amino acids. A peptide which mimics an antigenic fragment of the natural polypeptide may be fused with another protein such as keyhole hemolimpet cyanin (KLH; Sigma, St. Louis MO) for antibody production. A peptide
20 encompassing an antigenic region may be expressed from an mddt, synthesized as described above, or purified from human cells.

 Procedures well known in the art may be used for the production of antibodies. Various hosts including mice, goats, and rabbits, may be immunized by injection with a peptide. Depending on the host species, various adjuvants may be used to increase immunological response.

25 In one procedure, peptides about 15 residues in length may be synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel, 1995, supra). Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for anti-peptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin
30 (BSA), reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG. Antisera with anti-peptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, radioimmunoassay (RIA), and immunoblotting.

 In another procedure, isolated and purified peptide may be used to immunize mice (about 100 µg of peptide) or rabbits (about 1 mg of peptide). Subsequently, the peptide is radioiodinated and used

to screen the immunized animals' B-lymphocytes for production of anti-peptide antibodies. Positive cells are then used to produce hybridomas using standard techniques. About 20 mg of peptide is sufficient for labeling and screening several thousand clones. Hybridomas of interest are detected by screening with radioiodinated peptide to identify those fusions producing peptide-specific monoclonal antibody. In a typical protocol, wells of a multi-well plate (FAST, Becton-Dickinson, Palo Alto, CA) are coated with affinity-purified, specific rabbit-anti-mouse (or suitable anti-species IgG) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA and washed and exposed to supernatants from hybridomas. After incubation, the wells are exposed to radiolabeled peptide at 1 mg/ml.

Clones producing antibodies bind a quantity of labeled peptide that is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from the ascitic fluid by affinity chromatography on protein A (Amersham Pharmacia Biotech). Several procedures for the production of monoclonal antibodies, including *in vitro* production, are described in Pound (*supra*). Monoclonal antibodies with anti-peptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

Antibody fragments containing specific binding sites for an epitope may also be generated. For example, such fragments include, but are not limited to, the F(ab')₂ fragments produced by pepsin digestion of the antibody molecule, and the Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, construction of Fab expression libraries in filamentous bacteriophage allows rapid and easy identification of monoclonal fragments with desired specificity (Pound, *supra*, Chaps. 45-47). Antibodies generated against polypeptide encoded by mddt can be used to purify and characterize full-length MDDT protein and its activity, binding partners, etc.

Assays Using Antibodies

Anti-MDDT antibodies may be used in assays to quantify the amount of MDDT found in a particular human cell. Such assays include methods utilizing the antibody and a label to detect expression level under normal or disease conditions. The peptides and antibodies of the invention may be used with or without modification or labeled by joining them, either covalently or noncovalently, with a reporter molecule.

Protocols for detecting and measuring protein expression using either polyclonal or monoclonal antibodies are well known in the art. Examples include ELISA, RIA, and fluorescent activated cell sorting (FACS). Such immunoassays typically involve the formation of complexes between the MDDT and its specific antibody and the measurement of such complexes. These and other assays are described in Pound (*supra*).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

5 The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/185,213, U.S. Ser. No. 60/205,285, U.S. Ser. No. 60/205,232, U.S. Ser. No. 60/205,323, U.S. Ser. No. 60/205,287, U.S. Ser. No. 60/205,324, and U.S. Ser. No. 60/205,286, are hereby expressly incorporated by reference.

10

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from CLONTECH Laboratories, Inc. (Palo Alto CA) or isolated from various tissues. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life
15 Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA
purity. In most cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated
20 using oligo d(T)-coupled paramagnetic particles (Promega Corporation (Promega), Madison WI), OLIGOTEX latex particles (QIAGEN, Inc. (QIAGEN), Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Inc., Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA
25 libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene Cloning Systems, Inc. (Stratagene), La Jolla CA) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, *supra*, Chapters 5.1 through 6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double
30 stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid

(Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto CA), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

5

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: the Magic or WIZARD Minipreps DNA purification system (Promega); the AGTC Miniprep purification kit (Edge
10 BioSystems, Gaithersburg MD); and the QIAWELL 8, QIAWELL 8 Plus, and QIAWELL 8 Ultra plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit (QIAGEN). Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a
15 high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14.) Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Inc. (Molecular Probes), Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

20

III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 thermal cycler (Applied Biosystems) or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific
25 Corp., Sunnyvale CA) or the MICROLAB 2200 liquid transfer system (Hamilton). cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system
30 (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, Chapter 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

IV. Assembly and Analysis of Sequences

Component sequences from chromatograms were subject to PHRED analysis and assigned a quality score. The sequences having at least a required quality score were subject to various pre-processing editing pathways to eliminate, e.g., low quality 3' ends, vector and linker sequences, polyA
5 tails, Alu repeats, mitochondrial and ribosomal sequences, bacterial contamination sequences, and sequences smaller than 50 base pairs. In particular, low-information sequences and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) were replaced by "n's", or masked, to prevent spurious matches.

Processed sequences were then subject to assembly procedures in which the sequences were
10 assigned to gene bins (bins). Each sequence could only belong to one bin. Sequences in each gene bin were assembled to produce consensus sequences (templates). Subsequent new sequences were added to existing bins using BLASTn (v.1.4 WashU) and CROSSMATCH. Candidate pairs were identified as all BLAST hits having a quality score greater than or equal to 150. Alignments of at least 82% local identity were accepted into the bin. The component sequences from each bin were assembled using a
15 version of PHRAP. Bins with several overlapping component sequences were assembled using DEEP PHRAP. The orientation (sense or antisense) of each assembled template was determined based on the number and orientation of its component sequences. Template sequences as disclosed in the sequence listing correspond to sense strand sequences (the "forward" reading frames), to the best determination. The complementary (antisense) strands are inherently disclosed herein. The component sequences
20 which were used to assemble each template consensus sequence are listed in Table 4, along with their positions along the template nucleotide sequences.

Bins were compared against each other and those having local similarity of at least 82% were combined and reassembled. Reassembled bins having templates of insufficient overlap (less than 95% local identity) were re-split. Assembled templates were also subject to analysis by STITCHER/EXON
25 MAPPER algorithms which analyze the probabilities of the presence of splice variants, alternatively spliced exons, splice junctions, differential expression of alternative spliced genes across tissue types or disease states, etc. These resulting bins were subject to several rounds of the above assembly procedures.

Once gene bins were generated based upon sequence alignments, bins were clone joined based
30 upon clone information. If the 5' sequence of one clone was present in one bin and the 3' sequence from the same clone was present in a different bin, it was likely that the two bins actually belonged together in a single bin. The resulting combined bins underwent assembly procedures to regenerate the consensus sequences.

The final assembled templates were subsequently annotated using the following procedure. Template sequences were analyzed using BLASTn (v2.0, NCBI) versus gbpri (GenBank version 120). "Hits" were defined as an exact match having from 95% local identity over 200 base pairs through 100% local identity over 100 base pairs, or a homolog match having an E-value, i.e. a probability score, of $\leq 1 \times 10^{-8}$. The hits were subject to frameshift FASTx versus GENPEPT (GenBank version 5 120). (See Table 7). In this analysis, a homolog match was defined as having an E-value of $\leq 1 \times 10^{-8}$. The assembly method used above was described in "System and Methods for Analyzing Biomolecular Sequences," U.S.S.N. 09/276,534, filed March 25, 1999, and the LIFESEQ Gold user manual (Incyte) both incorporated by reference herein.

10 Following assembly, template sequences were subjected to motif, BLAST, and functional analyses, and categorized in protein hierarchies using methods described in, e.g., "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S.S.N. 08/812,290, filed March 6, 1997; "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence 15 Database," U.S.S.N. 08/811,758, filed March 6, 1997; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein.

The template sequences were further analyzed by translating each template in all three forward reading frames and searching each translation against the Pfam database of hidden Markov model- 20 based protein families and domains using the HMMER software package (available to the public from Washington University School of Medicine, St. Louis MO). Regions of templates which, when translated, contain similarity to Pfam consensus sequences are reported in Table 2, along with descriptions of Pfam protein domains and families. Only those Pfam hits with an E-value of $\leq 1 \times 10^{-3}$ are reported. (See also World Wide Web site <http://pfam.wustl.edu/> for detailed descriptions of Pfam 25 protein domains and families.)

Additionally, the template sequences were translated in all three forward reading frames, and each translation was searched against hidden Markov models for signal peptides using the HMMER software package. Construction of hidden Markov models and their usage in sequence analysis has been described. (See, for example, Eddy, S.R. (1996) *Curr. Opin. Str. Biol.* 6:361-365.) Only those 30 signal peptide hits with a cutoff score of 11 bits or greater are reported. A cutoff score of 11 bits or greater corresponds to at least about 91-94% true-positives in signal peptide prediction. Template sequences were also translated in all three forward reading frames, and each translation was searched against TMAP, a program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation, with respect to the cell cytosol (Persson, B. and P. Argos (1994) J.

Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.) Regions of templates which, when translated, contain similarity to signal peptide or transmembrane consensus sequences are reported in Table 3.

The results of HMMER analysis as reported in Tables 2 and 3 may support the results of
5 BLAST analysis as reported in Table 1 or may suggest alternative or additional properties of template-
encoded polypeptides not previously uncovered by BLAST or other analyses.

Template sequences are further analyzed using the bioinformatics tools listed in Table 7, or
using sequence analysis software known in the art such as MACDNASIS PRO software (Hitachi
Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Template
10 sequences may be further queried against public databases such as the GenBank rodent, mammalian,
vertebrate, prokaryote, and eukaryote databases.

The template sequences were translated to derive the corresponding longest open reading frame
as presented by the polypeptide sequences. Alternatively, a polypeptide of the invention may begin at
any of the methionine residues within the full length translated polypeptide. Polypeptide sequences
15 were subsequently analyzed by querying against the GenBank protein database (GENPEPT, (GenBank
version 121)). Full length polynucleotide sequences are also analyzed using MACDNASIS PRO
software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software
(DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default
parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence
20 alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 6 shows sequences with homology to the polypeptides of the invention as identified by
BLAST analysis against the GenBank protein (GENPEPT) database. Column 1 shows the polypeptide
sequence identification number (SEQ ID NO:) for the polypeptide segments of the invention. Column 2
shows the reading frame used in the translation of the polynucleotide sequences encoding the
25 polypeptide segments. Column 3 shows the length of the translated polypeptide segments. Columns 4
and 5 show the start and stop nucleotide positions of the polynucleotide sequences encoding the
polypeptide segments. Column 6 shows the GenBank identification number (GI Number) of the nearest
GenBank homolog. Column 7 shows the probability score for the match between each polypeptide and
its GenBank homolog. Column 8 shows the annotation of the GenBank homolog.

30 V. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene
and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a
particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995,
supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar.

- 5 The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{\text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2})\}}$$

- 10 The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.
- 15
20

VI. Tissue Distribution Profiling

- A tissue distribution profile is determined for each template by compiling the cDNA library tissue classifications of its component cDNA sequences. Each component sequence, is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. Template sequences, component sequences, and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).
- 25
30

Table 5 shows the tissue distribution profile for the templates of the invention. For each template, the three most frequently observed tissue categories are shown in column 3, along with the

percentage of component sequences belonging to each category. Only tissue categories with percentage values of $\geq 10\%$ are shown. A tissue distribution of "widely distributed" in column 3 indicates percentage values of $<10\%$ in all tissue categories.

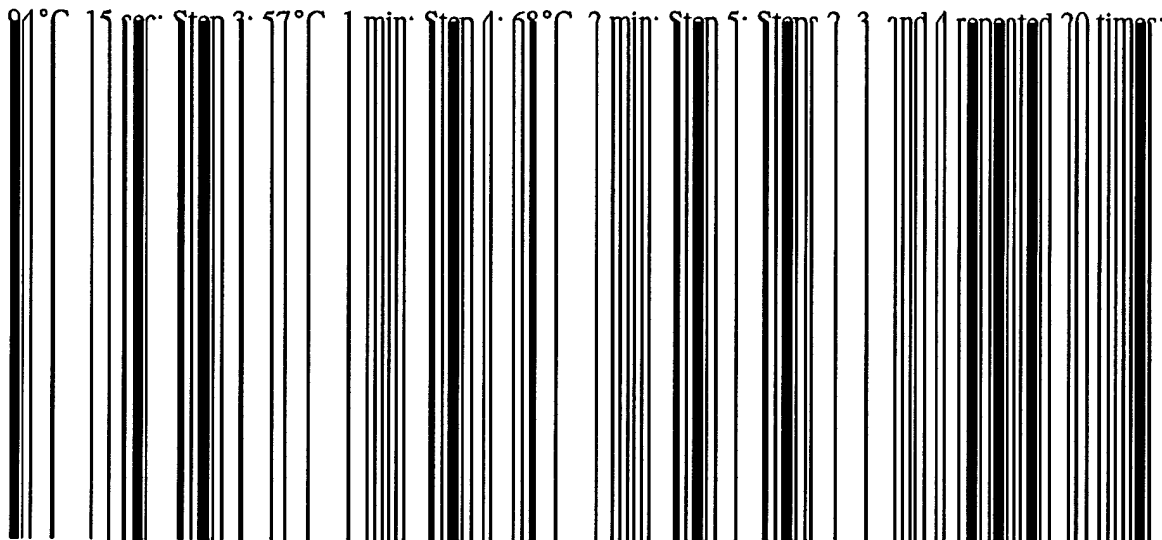
5 **VII. Transcript Image Analysis**

Transcript images are generated as described in Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, incorporated herein by reference.

VIII. Extension of Polynucleotide Sequences and Isolation of a Full-length cDNA

10 Oligonucleotide primers designed using an mddt of the Sequence Listing are used to extend the nucleic acid sequence. One primer is synthesized to initiate 5' extension of the template, and the other primer, to initiate 3' extension of the template. The initial primers may be designed using OLIGO 4.06 software (National Biosciences, Inc. (National Biosciences), Plymouth MN), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to
 15 anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations are avoided. Selected human cDNA libraries are used to extend the sequence. If more than one extension is necessary or desired, additional or nested sets of primers are designed.

High fidelity amplification is obtained by PCR using methods well known in the art. PCR is
 20 performed in 96-well plates using the PTC-200 thermal cycler (MJ Research). The reaction mix contains DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2
 25 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ are as follows: Step 1: 94°C, 3 min; Step 2:



to determine which reactions are successful in extending the sequence.

The extended nucleotides are desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For
5 shotgun sequencing, the digested nucleotides are separated on low concentration (0.6 to 0.8%) agarose gels, fragments are excised, and agar digested with AGAR ACE (Promega). Extended clones are religated using T4 ligase (New England Biolabs, Inc., Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells are selected on antibiotic-containing
10 media, individual colonies are picked and cultured overnight at 37°C in 384-well plates in LB/2x carbenicillin liquid media.

The cells are lysed, and DNA is amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4
15 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA is quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries are reamplified using the same conditions as described above. Samples are diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle
20 sequencing ready reaction kit (Applied Biosystems).

In like manner, the mddt is used to obtain regulatory sequences (promoters, introns, and enhancers) using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

25 IX. Labeling of Probes and Southern Hybridization Analyses

Hybridization probes derived from the mddt of the Sequence Listing are employed for screening cDNAs, mRNAs, or genomic DNA. The labeling of probe nucleotides between 100 and 1000 nucleotides in length is specifically described, but essentially the same procedure may be used with larger cDNA fragments. Probe sequences are labeled at room temperature for 30 minutes using a
30 T4 polynucleotide kinase, $\gamma^{32}\text{P}$ -ATP, and 0.5X One-Phor-All Plus (Amersham Pharmacia Biotech) buffer and purified using a ProbeQuant G-50 Microcolumn (Amersham Pharmacia Biotech). The probe mixture is diluted to 10^7 dpm/ $\mu\text{g/ml}$ hybridization buffer and used in a typical membrane-based hybridization analysis.

The DNA is digested with a restriction endonuclease such as Eco RV and is electrophoresed

through a 0.7% agarose gel. The DNA fragments are transferred from the agarose to nylon membrane (NYTRAN Plus, Schleicher & Schuell, Inc., Keene NH) using procedures specified by the manufacturer of the membrane. Prehybridization is carried out for three or more hours at 68°C, and hybridization is carried out overnight at 68°C. To remove non-specific signals, blots are sequentially washed at room temperature under increasingly stringent conditions, up to 0.1x saline sodium citrate (SSC) and 0.5% sodium dodecyl sulfate. After the blots are placed in a PHOSPHORIMAGER cassette (Molecular Dynamics) or are exposed to autoradiography film, hybridization patterns of standard and experimental lanes are compared. Essentially the same procedure is employed when screening RNA.

10 X. Chromosome Mapping of mddt

The cDNA sequences which were used to assemble SEQ ID NO:1-45 are compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that match SEQ ID NO:1-45 are assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as PHRAP (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon are used to determine if any of the clustered sequences have been previously mapped. Inclusion of a mapped sequence in a cluster will result in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location. The genetic map locations of SEQ ID NO:1-45 are described as ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters.

XI. Microarray Analysis

Probe Preparation from Tissue or Cell Samples

30 Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and polyA⁺ RNA is purified using the oligo (dT) cellulose method. Each polyA⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/μl oligo-dT primer (21mer), 1X first strand buffer, 0.03 units/μl RNase inhibitor, 500 μM dATP, 500 μM dGTP, 500 μM dTTP, 40 μM dCTP, 40 μM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription

reaction is performed in a 25 ml volume containing 200 ng polyA⁺ RNA with GEMBRIGHT kits (Incyte). Specific control polyA⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA (W. Lei, unpublished). As quantitative controls, the control mRNAs at 0.002 ng, 0.02 ng, 0.2 ng, and 2 ng are diluted into reverse transcription reaction at ratios of 1:100,000, 1:10,000, 5 1:1000, 1:100 (w/w) to sample mRNA respectively. The control mRNAs are diluted into reverse transcription reaction at ratios of 1:3, 3:1, 1:10, 10:1, 1:25, 25:1 (w/w) to sample mRNA differential expression patterns. After incubation at 37° C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85° C to stop the reaction and degrade the RNA. Probes are purified using two successive 10 CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The probe is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 µl 5X SSC/0.2% SDS.

15

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are 20 amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 µg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific 25 Products Corporation (VWR), West Chester, PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic 30 apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford, MA) for 30 minutes at 60° C followed by washes in 0.2%

SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 μ l of probe mixture consisting of 0.2 μ g each of Cy3 and
5 Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The probe mixture
is heated to 65° C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8
cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger
than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μ l of
5x SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5
1.0 hours at 60° C. The arrays are washed for 10 min at 45° C in a first wash buffer (1X SSC, 0.1% SDS),
three times for 10 minutes each at 45° C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an
15 Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines
at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is
focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide
containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-
scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a
2.0 resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially.
Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477,
Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate
filters positioned between the array and the photomultiplier tubes are used to filter the signals. The
2.5 emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is
typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source,
although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a
cDNA control species added to the probe mix at a known concentration. A specific location on the
3.0 array contains a complementary DNA sequence, allowing the intensity of the signal at that location to
be correlated with a weight ratio of hybridizing species of 1:100,000. When two probes from different
sources (e.g., representing test and control cells), each labeled with a different fluorophore,
are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the

calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood, MA) installed in an IBM-compatible PC
5 computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

10 A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

15 XII. Complementary Nucleic Acids

Sequences complementary to the mddt are used to detect, decrease, or inhibit expression of the naturally occurring nucleotide. The use of oligonucleotides comprising from about 15 to 30 base pairs is typical in the art. However, smaller or larger sequence fragments can also be used. Appropriate oligonucleotides are designed from the mddt using OLIGO 4.06 software (National Biosciences) or
20 other appropriate programs and are synthesized using methods standard in the art or ordered from a commercial supplier. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent transcription factor binding to the promoter sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding and processing of the transcript.

25

XIII. Expression of MDDT

Expression and purification of MDDT is accomplished using bacterial or virus-based expression systems. For expression of MDDT in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of
30 cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express MDDT upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of MDDT in eukaryotic cells is achieved by infecting insect

or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding MDDT by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See e.g., Engelhard, supra; and Sandig, supra.)

In most expression systems, MDDT is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from MDDT at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak Company, Rochester NY). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, Chapters 10 and 16). Purified MDDT obtained by these methods can be used directly in the following activity assay.

XIV. Demonstration of MDDT Activity

MDDT, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled MDDT, washed, and any wells with labeled MDDT complex are assayed. Data obtained using different concentrations of MDDT are used to calculate values for the number, affinity, and association of MDDT with the candidate molecules.

Alternatively, molecules interacting with MDDT are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) *Nature* 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (CLONTECH).

MDDT may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions

between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XV. Functional Assays

5 MDDT function is assessed by expressing mddt at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen Corporation, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell
10 line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected.

Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector.
15 Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; CLONTECH), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties.

FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding
20 or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane
25 composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) *Flow Cytometry*, Oxford, New York NY.

The influence of MDDT on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding MDDT and either CD64 or CD64-GFP. CD64 and
30 CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Inc., Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art.

Expression of mRNA encoding MDDT and other genes of interest can be analyzed by northern analysis or microarray techniques.

XVI. Production of Antibodies

5 MDDT substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the MDDT amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding peptide is synthesized
10 and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, Chapter 11.)

Typically, peptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with
15 N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, *supra*.) Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-MDDT activity
20 using protocols well known in the art, including ELISA, RIA, and immunoblotting.

XVII. Purification of Naturally Occurring MDDT Using Specific Antibodies

Naturally occurring or recombinant MDDT is substantially purified by immunoaffinity chromatography using antibodies specific for MDDT. An immunoaffinity column is constructed by
25 covalently coupling anti-MDDT antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing MDDT are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of MDDT (e.g., high ionic strength
30 buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/MDDT binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and MDDT is collected.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should
5 be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

10

TABLE 1

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
1	LG:977683.1:2000FEB18	g10764778	0	phosphoinositol 3-phosphate-binding protein-2 (Homo sapiens)
2	LG:893050.1:2000FEB18	g6634025	2.00E-81	KIAA0379 protein (Homo sapiens)
3	LG:980153.1:2000FEB18	g7263990	0	dJ93K22.1 (novel protein (contains DKFZP564B116)) (Homo sapiens)
4	LG:350398.1:2000FEB18	g3882175	3.00E-10	KIAA0727 protein (Homo sapiens)
5	LG:475551.1:2000FEB18	g861029	0	SH3 domain binding protein (Mus musculus)
6	LG:481407.2:2000FEB18	g6119546	1.00E-41	hypothetical protein; 114721-113936 (Arabidopsis thaliana)
7	LI:443580.1:2000FEB01	g4589566	3.00E-34	KIAA0961 protein (Homo sapiens)
8	LI:803015.1:2000FEB01	g5262560	2.00E-35	hypothetical protein (Homo sapiens)
9	LG:027410.3:2000MAY19	g10438267	1.00E-65	unnamed protein product (Homo sapiens)
10	LG:171377.1:2000MAY19	g3077703	1.00E-107	mitsugumin29 (Oryctolagus cuniculus)
11	LG:352559.1:2000MAY19	g7243243	2.00E-43	KIAA1431 protein (Homo sapiens)
12	LG:247384.1:2000MAY19	g9945010	1.00E-118	RING-finger protein MURF (Mus musculus)
13	LG:403872.1:2000MAY19	g7020303	0	unnamed protein product (Homo sapiens)
14	LG:1135213.1:2000MAY19	g6692607	2.00E-65	MGA protein (Mus musculus)
15	LG:474284.2:2000MAY19	g1488047	2.00E-30	RING finger protein (Xenopus laevis)
16	LG:342147.1:2000MAY19	g2477511	3.00E-41	Homo sapiens p20 protein (pir B53814)
17	LG:1097300.1:2000MAY19	g2078531	1.00E-70	Mlark (Mus musculus)
18	LG:444850.9:2000MAY19	g199000	0	interferon-gamma inducible protein (Mus musculus)
19	LG:402231.6:2000MAY19	g7020737	6.00E-77	unnamed protein product (Homo sapiens)
20	LG:1076157.1:2000MAY19	g5262560	3.00E-65	hypothetical protein (Homo sapiens)
21	LG:1083142.1:2000MAY19	g4589566	3.00E-23	KIAA0961 protein (Homo sapiens)
22	LG:1083264.1:2000MAY19	g10047297	2.00E-25	KIAA1611 protein (Homo sapiens)
23	LG:350793.2:2000MAY19	g7242973	0	KIAA1309 protein (Homo sapiens)
24	LG:408751.3:2000MAY19	g8886025	1.00E-134	collapse response mediator protein-5 (Homo sapiens)
25	LI:336120.1:2000MAY01	g1864085	1.00E-160	glypican-5 (Homo sapiens)
26	LI:234104.2:2000MAY01	g1518505	1.00E-114	G-protein coupled inwardly rectifying K+ channel (Mus musculus)
27	LI:450887.1:2000MAY01	g7629994	3.00E-34	60S RIBOSOMAL PROTEIN L36 homolog (Arabidopsis thaliana)
28	LI:119992.3:2000MAY01	g7243089	0	KIAA1354 protein (Homo sapiens)
29	LI:197241.2:2000MAY01	g7263990	0	dJ93K22.1 (novel protein (contains DKFZP564B116)) (Homo sapiens)
30	LI:406860.20:2000MAY01	g10435919	3.00E-57	unnamed protein product (Homo sapiens)

31	LI:142384.1:2000MAY01	g10436290	1.00E-131	unnamed protein product (Homo sapiens)
32	LI:895427.1:2000MAY01	g3184264	1.00E-106	F02569_2 (Homo sapiens)
33	LI:757439.1:2000MAY01	g7670362	1.00E-116	unnamed protein product (Mus musculus)
34	LI:1144066.1:2000MAY01	g3882281	7.00E-79	KIAA0780 protein (Homo sapiens)
35	LI:243660.4:2000MAY01	g4210501	0	BC85722_1 (Homo sapiens)
36	LI:334386.1:2000MAY01	g6330617	0	KIAA1223 protein (Homo sapiens)
37	LI:347572.1:2000MAY01	g9802433	1.00E-101	ACE-related carboxypeptidase ACE2 (Homo sapiens)
38	LI:817314.1:2000MAY01	g5802615	0	transient receptor potential 4 (Homo sapiens)
39	LI:000290.1:2000MAY01	g7242977	2.00E-51	KIAA1311 protein (Homo sapiens)
40	LI:023518.3:2000MAY01	g736727	2.00E-74	32 kd accessory protein (Bos taurus)
41	LI:1084246.1:2000MAY01	g5457031	0	protocadherin beta 12 (Homo sapiens)
42	LI:1165828.1:2000MAY01	g5457019	0	protocadherin alpha 7 short form protein (Homo sapiens)
43	LI:007302.1:2000MAY01	g5006250	0	TLR6 (Mus musculus)
44	LI:236386.4:2000MAY01	g6164628	1.00E-63	SH3 and PX domain-containing protein SH3PX1 (Homo sapiens)
45	LI:252904.5:2000MAY01	g7022971	2.00E-62	unnamed protein product (Homo sapiens)

TABLE 2

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
1	LG:977683.1:2000FEB18	540	695	forward 3	PH	PH domain	6.70E-11
1	LG:977683.1:2000FEB18	204	293	forward 3	WW	WW domain	7.50E-05
2	LG:893050.1:2000FEB18	211	309	forward 1	ank	Ank repeat	1.60E-05
3	LG:980153.1:2000FEB18	754	852	forward 1	ank	Ank repeat	8.00E-04
3	LG:980153.1:2000FEB18	2131	2565	forward 1	BTB	BTB/POZ domain	6.90E-07
3	LG:980153.1:2000FEB18	1084	1239	forward 1	RCC1	Regulator of chromosome condensation	3.70E-04
4	LG:350398.1:2000FEB18	7	123	forward 1	myosin_head	Myosin head (motor domain)	2.60E-16
5	LG:475551.1:2000FEB18	702	1157	forward 3	RhoGAP	RhoGAP domain	8.10E-71
6	LG:481407.2:2000FEB18	225	440	forward 3	rrm	RNA recognition motif. (a.k.a. RRM, RBC	1.50E-22
6	LG:481407.2:2000FEB18	504	557	forward 3	zf-CCHC	Zinc knuckle	7.00E-04
7	LI:443580.1:2000FEB01	262	450	forward 1	KRAB	KRAB box	1.60E-41
7	LI:443580.1:2000FEB01	625	693	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.20E-06
8	LI:803015.1:2000FEB01	159	299	forward 3	KRAB	KRAB box	2.30E-17
9	LG:027410.3:2000MAY19	177	290	forward 3	WD40	WD domain, G-beta repeat	6.20E-06
10	LG:171377.1:2000MAY19	300	848	forward 3	Synaptophysin	Synaptophysin / synaptoporin	2.10E-20
11	LG:352559.1:2000MAY19	125	313	forward 2	KRAB	KRAB box	1.60E-41
12	LG:247384.1:2000MAY19	182	256	forward 2	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.80E-06
13	LG:403872.1:2000MAY19	717	1187	forward 3	PAP2	PAP2 superfamily	1.80E-09
14	LG:1135213.1:2000MAY19	340	531	forward 1	T-box	T-box	8.80E-27
15	LG:474284.2:2000MAY19	73	195	forward 1	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.20E-13
16	LG:342147.1:2000MAY19	290	469	forward 2	crystallin	Alpha crystallin A chain, N terminal	3.10E-09
16	LG:342147.1:2000MAY19	452	628	forward 2	HSP20	Hsp20/alpha crystallin family	7.20E-12
17	LG:1097300.1:2000MAY19	59	250	forward 2	rrm	RNA recognition motif. (a.k.a. RRM, RBC	4.10E-16
18	LG:444850.9:2000MAY19	190	1290	forward 1	GBP	Guanylate-binding protein	4.20E-247
19	LG:402231.6:2000MAY19	258	380	forward 3	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.30E-05
20	LG:1076157.1:2000MAY19	180	320	forward 3	KRAB	KRAB box	3.40E-18
21	LG:1083142.1:2000MAY19	129	320	forward 3	KRAB	KRAB box	2.00E-42
22	LG:1083264.1:2000MAY19	440	628	forward 2	KRAB	KRAB box	2.30E-33
23	LG:350793.2:2000MAY19	570	722	forward 3	Keich	Keich motif	2.70E-11
24	LG:408751.3:2000MAY19	194	1051	forward 2	Dihydroorotase	Dihydroorotase-like	5.50E-07
25	LI:336120.1:2000MAY01	232	1398	forward 1	Glypican	Glypican	9.90E-141
25	LI:336120.1:2000MAY01	1476	1907	forward 3	Glypican	Glypican	8.60E-70
25	LI:336120.1:2000MAY01	503	775	forward 2	Glypican	Glypican	3.50E-46
26	LI:234104.2:2000MAY01	2517	3002	forward 3	IRK	Inward rectifier potassium channel	8.70E-111

26	LI:234104.2:2000MAY01	2965	3507	forward 1	IRK	Inward rectifier potassium channel	9.20E-111
27	LI:450887.1:2000MAY01	48	344	forward 3	Ribosomal_L36e	Ribosomal protein L36e	6.90E-41
28	LI:119992.3:2000MAY01	788	925	forward 2	Kelch	Kelch motif	1.50E-09
29	LI:197241.2:2000MAY01	1243	1407	forward 1	RCC1	Regulator of chromosome condensation	1.60E-04
30	LI:406860.20:2000MAY01	228	407	forward 3	ig	Immunoglobulin domain	1.90E-08
31	LI:142384.1:2000MAY01	318	791	forward 3	UQ_con	Ubiquitin-conjugating enzyme	1.40E-16
32	LI:895427.1:2000MAY01	437	907	forward 2	RhoGAP	RhoGAP domain	1.20E-40
33	LI:757439.1:2000MAY01	1040	1162	forward 2	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.20E-10
34	LI:1144066.1:2000MAY01	222	365	forward 3	jmjN	jmjN domain	2.80E-23
35	LI:243660.4:2000MAY01	316	522	forward 1	HMG_box	HMG (high mobility group) box	8.60E-17
36	LI:334386.1:2000MAY01	272	370	forward 2	ank	Ank repeat	4.90E-08
36	LI:334386.1:2000MAY01	735	833	forward 3	ank	Ank repeat	4.50E-05
37	LI:347572.1:2000MAY01	130	1878	forward 1	Peptidase_M2	Angiotensin-converting enzyme	2.60E-05
38	LI:817314.1:2000MAY01	934	2034	forward 1	Trans_recep	Transient receptor	6.50E-260
38	LI:817314.1:2000MAY01	1929	2321	forward 3	Trans_recep	Transient receptor	2.20E-81
39	LI:000290.1:2000MAY01	960	1040	forward 3	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type (and ε	7.70E-04
40	LI:023518.3:2000MAY01	195	845	forward 3	vATP-synt_AC39	ATP synthase (C/AC39) subunit	5.30E-38
41	LI:1084246.1:2000MAY01	1443	1733	forward 3	cadherin	Cadherin domain	2.30E-20
41	LI:1084246.1:2000MAY01	875	1150	forward 2	cadherin	Cadherin domain	6.60E-17
42	LI:1165828.1:2000MAY01	1421	1705	forward 2	cadherin	Cadherin domain	1.30E-19
43	LI:007302.1:2000MAY01	1646	1810	forward 2	LRRCT	Leucine rich repeat C-terminal domain	2.60E-13
43	LI:007302.1:2000MAY01	1991	2455	forward 2	TIR	TIR domain	3.50E-37
44	LI:236386.4:2000MAY01	677	850	forward 2	SH3	SH3 domain	5.20E-07
45	LI:252904.5:2000MAY01	358	495	forward 1	Kelch	Kelch motif	3.80E-07

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
1	LG:977683.1:2000FEB18	373	459	forward 1	TM	N in
1	LG:977683.1:2000FEB18	657	731	forward 3	TM	N out
2	LG:893050.1:2000FEB18	15	101	forward 3	TM	N out
3	LG:980153.1:2000FEB18	313	375	forward 1	TM	N out
3	LG:980153.1:2000FEB18	391	453	forward 1	TM	N out
3	LG:980153.1:2000FEB18	278	364	forward 2	TM	N out
3	LG:980153.1:2000FEB18	416	493	forward 2	TM	N out
3	LG:980153.1:2000FEB18	809	871	forward 2	TM	N out
3	LG:980153.1:2000FEB18	902	964	forward 2	TM	N out
3	LG:980153.1:2000FEB18	1181	1264	forward 2	TM	N out
3	LG:980153.1:2000FEB18	1427	1510	forward 2	TM	N out
3	LG:980153.1:2000FEB18	1733	1798	forward 2	TM	N out
3	LG:980153.1:2000FEB18	1868	1954	forward 2	TM	N out
3	LG:980153.1:2000FEB18	2141	2227	forward 2	TM	N out
3	LG:980153.1:2000FEB18	2261	2308	forward 2	TM	N out
3	LG:980153.1:2000FEB18	60	125	forward 3	TM	N in
3	LG:980153.1:2000FEB18	402	476	forward 3	TM	N in
3	LG:980153.1:2000FEB18	2031	2081	forward 3	TM	N in
3	LG:980153.1:2000FEB18	2142	2213	forward 3	TM	N in
5	LG:475551.1:2000FEB18	2134	2208	forward 1	TM	N in
5	LG:475551.1:2000FEB18	2039	2125	forward 2	TM	N out
5	LG:475551.1:2000FEB18	1167	1217	forward 3	TM	N in
6	LG:481407.2:2000FEB18	874	927	forward 1	TM	
6	LG:481407.2:2000FEB18	949	1035	forward 1	TM	
6	LG:481407.2:2000FEB18	1081	1161	forward 1	TM	
6	LG:481407.2:2000FEB18	1510	1584	forward 1	TM	
6	LG:481407.2:2000FEB18	1355	1435	forward 2	TM	N out
6	LG:481407.2:2000FEB18	1439	1525	forward 2	TM	N out
6	LG:481407.2:2000FEB18	1326	1409	forward 3	TM	N in
6	LG:481407.2:2000FEB18	1446	1526	forward 3	TM	N in
6	LG:481407.2:2000FEB18	1545	1616	forward 3	TM	N in
7	LI:443580.1:2000FEB01	488	574	forward 2	TM	N out
10	LG:171377.1:2000MAY19	318	386	forward 3	TM	N in
10	LG:171377.1:2000MAY19	549	635	forward 3	TM	N in
10	LG:171377.1:2000MAY19	669	740	forward 3	TM	N in
12	LG:247384.1:2000MAY19	1381	1461	forward 1	TM	N in
12	LG:247384.1:2000MAY19	1624	1710	forward 1	TM	N in
12	LG:247384.1:2000MAY19	1409	1495	forward 2	TM	N in
12	LG:247384.1:2000MAY19	1395	1481	forward 3	TM	N in
12	LG:247384.1:2000MAY19	1617	1679	forward 3	TM	N in
13	LG:403872.1:2000MAY19	535	621	forward 1	TM	N in
13	LG:403872.1:2000MAY19	1360	1446	forward 1	TM	N in
13	LG:403872.1:2000MAY19	1522	1581	forward 1	TM	N in
13	LG:403872.1:2000MAY19	1828	1902	forward 1	TM	N in
13	LG:403872.1:2000MAY19	1957	2022	forward 1	TM	N in
13	LG:403872.1:2000MAY19	299	349	forward 2	TM	N in
13	LG:403872.1:2000MAY19	1361	1423	forward 2	TM	N in
13	LG:403872.1:2000MAY19	1439	1501	forward 2	TM	N in
13	LG:403872.1:2000MAY19	1553	1627	forward 2	TM	N in
13	LG:403872.1:2000MAY19	1859	1918	forward 2	TM	N in
13	LG:403872.1:2000MAY19	2027	2110	forward 2	TM	N in
13	LG:403872.1:2000MAY19	2117	2203	forward 2	TM	N in
13	LG:403872.1:2000MAY19	369	452	forward 3	TM	N in

13	LG:403872.1:2000MAY19	549	635	forward 3	TM	N in
13	LG:403872.1:2000MAY19	708	785	forward 3	TM	N in
13	LG:403872.1:2000MAY19	1101	1187	forward 3	TM	N in
13	LG:403872.1:2000MAY19	1419	1505	forward 3	TM	N in
13	LG:403872.1:2000MAY19	1575	1661	forward 3	TM	N in
13	LG:403872.1:2000MAY19	2115	2192	forward 3	TM	N in
13	LG:403872.1:2000MAY19	2226	2273	forward 3	TM	N in
14	LG:1135213.1:2000MAY19	41	127	forward 2	TM	N out
14	LG:1135213.1:2000MAY19	215	274	forward 2	TM	N out
14	LG:1135213.1:2000MAY19	293	379	forward 2	TM	N out
14	LG:1135213.1:2000MAY19	389	475	forward 2	TM	N out
16	LG:342147.1:2000MAY19	142	204	forward 1	TM	N out
16	LG:342147.1:2000MAY19	171	251	forward 3	TM	N out
17	LG:1097300.1:2000MAY19	487	564	forward 1	TM	
17	LG:1097300.1:2000MAY19	805	891	forward 1	TM	
17	LG:1097300.1:2000MAY19	1372	1458	forward 1	TM	
17	LG:1097300.1:2000MAY19	668	754	forward 2	TM	N out
17	LG:1097300.1:2000MAY19	803	874	forward 2	TM	N out
17	LG:1097300.1:2000MAY19	1358	1441	forward 2	TM	N out
17	LG:1097300.1:2000MAY19	522	578	forward 3	TM	N in
17	LG:1097300.1:2000MAY19	750	836	forward 3	TM	N in
17	LG:1097300.1:2000MAY19	894	956	forward 3	TM	N in
17	LG:1097300.1:2000MAY19	1068	1145	forward 3	TM	N in
18	LG:444850.9:2000MAY19	253	315	forward 1	TM	N in
19	LG:402231.6:2000MAY19	407	484	forward 2	TM	N in
23	LG:350793.2:2000MAY19	148	222	forward 1	TM	N in
23	LG:350793.2:2000MAY19	316	384	forward 1	TM	N in
23	LG:350793.2:2000MAY19	1144	1215	forward 1	TM	N in
23	LG:350793.2:2000MAY19	1231	1293	forward 1	TM	N in
23	LG:350793.2:2000MAY19	1339	1425	forward 1	TM	N in
23	LG:350793.2:2000MAY19	1459	1521	forward 1	TM	N in
23	LG:350793.2:2000MAY19	1582	1662	forward 1	TM	N in
23	LG:350793.2:2000MAY19	1882	1953	forward 1	TM	N in
23	LG:350793.2:2000MAY19	1514	1600	forward 2	TM	
23	LG:350793.2:2000MAY19	2135	2221	forward 2	TM	
23	LG:350793.2:2000MAY19	1422	1493	forward 3	TM	
23	LG:350793.2:2000MAY19	2268	2354	forward 3	TM	
24	LG:408751.3:2000MAY19	1202	1264	forward 2	TM	N out
24	LG:408751.3:2000MAY19	1137	1223	forward 3	TM	N in
25	LI:336120.1:2000MAY01	241	297	forward 1	TM	N in
25	LI:336120.1:2000MAY01	616	702	forward 1	TM	N in
25	LI:336120.1:2000MAY01	1141	1200	forward 1	TM	N in
25	LI:336120.1:2000MAY01	2524	2598	forward 1	TM	N in
25	LI:336120.1:2000MAY01	1163	1213	forward 2	TM	N in
25	LI:336120.1:2000MAY01	1922	1972	forward 2	TM	N in
25	LI:336120.1:2000MAY01	2060	2119	forward 2	TM	N in
25	LI:336120.1:2000MAY01	2510	2596	forward 2	TM	N in
25	LI:336120.1:2000MAY01	663	749	forward 3	TM	N in
25	LI:336120.1:2000MAY01	1380	1445	forward 3	TM	N in
25	LI:336120.1:2000MAY01	1839	1925	forward 3	TM	N in
25	LI:336120.1:2000MAY01	2148	2234	forward 3	TM	N in
25	LI:336120.1:2000MAY01	2418	2471	forward 3	TM	N in
25	LI:336120.1:2000MAY01	2499	2585	forward 3	TM	N in
26	LI:234104.2:2000MAY01	1873	1947	forward 1	TM	N out
26	LI:234104.2:2000MAY01	2155	2241	forward 1	TM	N out
26	LI:234104.2:2000MAY01	3616	3690	forward 1	TM	N out

26	LI:234104.2:2000MAY01	1112	1168	forward 2	TM	N in
26	LI:234104.2:2000MAY01	2216	2302	forward 2	TM	N in
26	LI:234104.2:2000MAY01	3632	3718	forward 2	TM	N in
26	LI:234104.2:2000MAY01	3998	4045	forward 2	TM	N in
26	LI:234104.2:2000MAY01	1314	1400	forward 3	TM	N in
26	LI:234104.2:2000MAY01	2172	2258	forward 3	TM	N in
26	LI:234104.2:2000MAY01	2607	2684	forward 3	TM	N in
26	LI:234104.2:2000MAY01	2739	2798	forward 3	TM	N in
26	LI:234104.2:2000MAY01	2841	2891	forward 3	TM	N in
26	LI:234104.2:2000MAY01	3621	3707	forward 3	TM	N in
26	LI:234104.2:2000MAY01	4080	4145	forward 3	TM	N in
28	LI:119992.3:2000MAY01	22	102	forward 1	TM	N out
28	LI:119992.3:2000MAY01	151	237	forward 1	TM	N out
28	LI:119992.3:2000MAY01	1444	1530	forward 1	TM	N out
28	LI:119992.3:2000MAY01	1603	1683	forward 1	TM	N out
28	LI:119992.3:2000MAY01	1729	1809	forward 1	TM	N out
28	LI:119992.3:2000MAY01	2197	2253	forward 1	TM	N out
28	LI:119992.3:2000MAY01	2269	2355	forward 1	TM	N out
28	LI:119992.3:2000MAY01	2989	3075	forward 1	TM	N out
28	LI:119992.3:2000MAY01	3163	3249	forward 1	TM	N out
28	LI:119992.3:2000MAY01	1247	1333	forward 2	TM	N in
28	LI:119992.3:2000MAY01	1538	1606	forward 2	TM	N in
28	LI:119992.3:2000MAY01	2207	2293	forward 2	TM	N in
28	LI:119992.3:2000MAY01	2756	2812	forward 2	TM	N in
28	LI:119992.3:2000MAY01	3098	3169	forward 2	TM	N in
28	LI:119992.3:2000MAY01	3281	3343	forward 2	TM	N in
28	LI:119992.3:2000MAY01	3356	3418	forward 2	TM	N in
28	LI:119992.3:2000MAY01	120	188	forward 3	TM	N in
28	LI:119992.3:2000MAY01	627	689	forward 3	TM	N in
28	LI:119992.3:2000MAY01	708	770	forward 3	TM	N in
28	LI:119992.3:2000MAY01	1425	1511	forward 3	TM	N in
28	LI:119992.3:2000MAY01	1782	1868	forward 3	TM	N in
28	LI:119992.3:2000MAY01	2223	2306	forward 3	TM	N in
28	LI:119992.3:2000MAY01	2757	2843	forward 3	TM	N in
28	LI:119992.3:2000MAY01	3027	3113	forward 3	TM	N in
28	LI:119992.3:2000MAY01	3213	3275	forward 3	TM	N in
28	LI:119992.3:2000MAY01	3312	3374	forward 3	TM	N in
29	LI:197241.2:2000MAY01	289	369	forward 1	TM	N out
29	LI:197241.2:2000MAY01	430	507	forward 1	TM	N out
29	LI:197241.2:2000MAY01	799	861	forward 1	TM	N out
29	LI:197241.2:2000MAY01	889	951	forward 1	TM	N out
29	LI:197241.2:2000MAY01	1798	1863	forward 1	TM	N out
29	LI:197241.2:2000MAY01	1930	2016	forward 1	TM	N out
29	LI:197241.2:2000MAY01	2101	2148	forward 1	TM	N out
29	LI:197241.2:2000MAY01	2206	2262	forward 1	TM	N out
29	LI:197241.2:2000MAY01	416	499	forward 2	TM	N out
29	LI:197241.2:2000MAY01	812	862	forward 2	TM	N out
29	LI:197241.2:2000MAY01	1226	1309	forward 2	TM	N out
29	LI:197241.2:2000MAY01	1475	1558	forward 2	TM	N out
29	LI:197241.2:2000MAY01	2210	2296	forward 2	TM	N out
29	LI:197241.2:2000MAY01	60	125	forward 3	TM	N in
29	LI:197241.2:2000MAY01	333	395	forward 3	TM	N in
29	LI:197241.2:2000MAY01	441	503	forward 3	TM	N in
29	LI:197241.2:2000MAY01	2223	2300	forward 3	TM	N in
31	LI:142384.1:2000MAY01	367	432	forward 1	TM	N out
31	LI:142384.1:2000MAY01	93	155	forward 3	TM	N out

32	LI:895427.1:2000MAY01	1796	1879	forward 2	TM	N in
32	LI:895427.1:2000MAY01	1656	1724	forward 3	TM	N in
33	LI:757439.1:2000MAY01	253	312	forward 1	TM	N in
33	LI:757439.1:2000MAY01	817	900	forward 1	TM	N in
33	LI:757439.1:2000MAY01	1507	1572	forward 1	TM	N in
33	LI:757439.1:2000MAY01	1615	1677	forward 1	TM	N in
33	LI:757439.1:2000MAY01	1696	1758	forward 1	TM	N in
33	LI:757439.1:2000MAY01	1834	1899	forward 1	TM	N in
33	LI:757439.1:2000MAY01	1969	2043	forward 1	TM	N in
33	LI:757439.1:2000MAY01	2107	2193	forward 1	TM	N in
33	LI:757439.1:2000MAY01	2506	2586	forward 1	TM	N in
33	LI:757439.1:2000MAY01	815	901	forward 2	TM	N out
33	LI:757439.1:2000MAY01	1634	1720	forward 2	TM	N out
33	LI:757439.1:2000MAY01	1796	1882	forward 2	TM	N out
33	LI:757439.1:2000MAY01	1952	2026	forward 2	TM	N out
33	LI:757439.1:2000MAY01	2486	2563	forward 2	TM	N out
33	LI:757439.1:2000MAY01	783	869	forward 3	TM	N in
33	LI:757439.1:2000MAY01	996	1049	forward 3	TM	N in
33	LI:757439.1:2000MAY01	1545	1631	forward 3	TM	N in
33	LI:757439.1:2000MAY01	2115	2174	forward 3	TM	N in
35	LI:243660.4:2000MAY01	1247	1333	forward 2	TM	N in
36	LI:334386.1:2000MAY01	538	621	forward 1	TM	
36	LI:334386.1:2000MAY01	922	1008	forward 1	TM	
36	LI:334386.1:2000MAY01	1087	1173	forward 1	TM	
36	LI:334386.1:2000MAY01	1468	1530	forward 1	TM	
36	LI:334386.1:2000MAY01	1570	1632	forward 1	TM	
36	LI:334386.1:2000MAY01	2731	2802	forward 1	TM	
36	LI:334386.1:2000MAY01	2992	3054	forward 1	TM	
36	LI:334386.1:2000MAY01	3325	3387	forward 1	TM	
36	LI:334386.1:2000MAY01	3406	3468	forward 1	TM	
36	LI:334386.1:2000MAY01	3487	3570	forward 1	TM	
36	LI:334386.1:2000MAY01	3766	3852	forward 1	TM	
36	LI:334386.1:2000MAY01	4006	4077	forward 1	TM	
36	LI:334386.1:2000MAY01	4342	4416	forward 1	TM	
36	LI:334386.1:2000MAY01	4615	4686	forward 1	TM	
36	LI:334386.1:2000MAY01	4747	4833	forward 1	TM	
36	LI:334386.1:2000MAY01	5062	5124	forward 1	TM	
36	LI:334386.1:2000MAY01	5140	5202	forward 1	TM	
36	LI:334386.1:2000MAY01	5227	5289	forward 1	TM	
36	LI:334386.1:2000MAY01	5563	5649	forward 1	TM	
36	LI:334386.1:2000MAY01	1235	1321	forward 2	TM	N in
36	LI:334386.1:2000MAY01	2423	2476	forward 2	TM	N in
36	LI:334386.1:2000MAY01	2702	2764	forward 2	TM	N in
36	LI:334386.1:2000MAY01	2792	2854	forward 2	TM	N in
36	LI:334386.1:2000MAY01	3086	3172	forward 2	TM	N in
36	LI:334386.1:2000MAY01	3302	3355	forward 2	TM	N in
36	LI:334386.1:2000MAY01	3452	3517	forward 2	TM	N in
36	LI:334386.1:2000MAY01	3920	4006	forward 2	TM	N in
36	LI:334386.1:2000MAY01	4064	4144	forward 2	TM	N in
36	LI:334386.1:2000MAY01	4250	4318	forward 2	TM	N in
36	LI:334386.1:2000MAY01	4331	4402	forward 2	TM	N in
36	LI:334386.1:2000MAY01	4523	4576	forward 2	TM	N in
36	LI:334386.1:2000MAY01	4586	4669	forward 2	TM	N in
36	LI:334386.1:2000MAY01	4772	4855	forward 2	TM	N in
36	LI:334386.1:2000MAY01	5039	5125	forward 2	TM	N in
36	LI:334386.1:2000MAY01	5498	5584	forward 2	TM	N in

36	LI:334386.1:2000MAY01	30	116	forward 3	TM	N in
36	LI:334386.1:2000MAY01	324	380	forward 3	TM	N in
36	LI:334386.1:2000MAY01	387	470	forward 3	TM	N in
36	LI:334386.1:2000MAY01	531	608	forward 3	TM	N in
36	LI:334386.1:2000MAY01	1362	1448	forward 3	TM	N in
36	LI:334386.1:2000MAY01	1539	1625	forward 3	TM	N in
36	LI:334386.1:2000MAY01	2232	2279	forward 3	TM	N in
36	LI:334386.1:2000MAY01	2580	2651	forward 3	TM	N in
36	LI:334386.1:2000MAY01	2757	2822	forward 3	TM	N in
36	LI:334386.1:2000MAY01	2820	2870	forward 3	TM	N in
36	LI:334386.1:2000MAY01	3282	3368	forward 3	TM	N in
36	LI:334386.1:2000MAY01	3510	3596	forward 3	TM	N in
36	LI:334386.1:2000MAY01	3981	4064	forward 3	TM	N in
36	LI:334386.1:2000MAY01	4356	4427	forward 3	TM	N in
36	LI:334386.1:2000MAY01	4464	4544	forward 3	TM	N in
36	LI:334386.1:2000MAY01	4959	5024	forward 3	TM	N in
36	LI:334386.1:2000MAY01	5601	5687	forward 3	TM	N in
37	LI:347572.1:2000MAY01	790	876	forward 1	TM	N in
37	LI:347572.1:2000MAY01	1354	1434	forward 1	TM	N in
37	LI:347572.1:2000MAY01	2425	2511	forward 1	TM	N in
37	LI:347572.1:2000MAY01	2599	2685	forward 1	TM	N in
37	LI:347572.1:2000MAY01	2686	2757	forward 1	TM	N in
37	LI:347572.1:2000MAY01	3133	3207	forward 1	TM	N in
37	LI:347572.1:2000MAY01	1184	1255	forward 2	TM	
37	LI:347572.1:2000MAY01	2264	2350	forward 2	TM	
37	LI:347572.1:2000MAY01	2597	2665	forward 2	TM	
37	LI:347572.1:2000MAY01	2942	3028	forward 2	TM	
37	LI:347572.1:2000MAY01	3137	3199	forward 2	TM	
37	LI:347572.1:2000MAY01	3227	3289	forward 2	TM	
37	LI:347572.1:2000MAY01	129	215	forward 3	TM	N in
37	LI:347572.1:2000MAY01	969	1046	forward 3	TM	N in
37	LI:347572.1:2000MAY01	1947	2033	forward 3	TM	N in
37	LI:347572.1:2000MAY01	2208	2288	forward 3	TM	N in
37	LI:347572.1:2000MAY01	2412	2477	forward 3	TM	N in
37	LI:347572.1:2000MAY01	2604	2684	forward 3	TM	N in
37	LI:347572.1:2000MAY01	2739	2795	forward 3	TM	N in
38	LI:817314.1:2000MAY01	460	546	forward 1	TM	
38	LI:817314.1:2000MAY01	1192	1278	forward 1	TM	
38	LI:817314.1:2000MAY01	1318	1386	forward 1	TM	
38	LI:817314.1:2000MAY01	1423	1485	forward 1	TM	
38	LI:817314.1:2000MAY01	1537	1599	forward 1	TM	
38	LI:817314.1:2000MAY01	1630	1692	forward 1	TM	
38	LI:817314.1:2000MAY01	1756	1842	forward 1	TM	
38	LI:817314.1:2000MAY01	1930	1992	forward 1	TM	
38	LI:817314.1:2000MAY01	2032	2094	forward 1	TM	
38	LI:817314.1:2000MAY01	2860	2946	forward 1	TM	
38	LI:817314.1:2000MAY01	3127	3213	forward 1	TM	
38	LI:817314.1:2000MAY01	362	448	forward 2	TM	N in
38	LI:817314.1:2000MAY01	3158	3244	forward 2	TM	N in
38	LI:817314.1:2000MAY01	30	95	forward 3	TM	N out
38	LI:817314.1:2000MAY01	1239	1301	forward 3	TM	N out
38	LI:817314.1:2000MAY01	1785	1865	forward 3	TM	N out
38	LI:817314.1:2000MAY01	1920	2000	forward 3	TM	N out
38	LI:817314.1:2000MAY01	3189	3269	forward 3	TM	N out
39	LI:000290.1:2000MAY01	1003	1065	forward 1	TM	N in
39	LI:000290.1:2000MAY01	1075	1137	forward 1	TM	N in

39	LI:000290.1:2000MAY01	1195	1248	forward 1	TM	N in
39	LI:000290.1:2000MAY01	767	844	forward 2	TM	
39	LI:000290.1:2000MAY01	882	932	forward 3	TM	N in
40	LI:023518.3:2000MAY01	28	108	forward 1	TM	N out
40	LI:023518.3:2000MAY01	20	106	forward 2	TM	N in
41	LI:1084246.1:2000MAY01	178	264	forward 1	TM	N out
41	LI:1084246.1:2000MAY01	2686	2760	forward 1	TM	N out
41	LI:1084246.1:2000MAY01	2932	3003	forward 1	TM	N out
41	LI:1084246.1:2000MAY01	3097	3159	forward 1	TM	N out
41	LI:1084246.1:2000MAY01	3184	3246	forward 1	TM	N out
41	LI:1084246.1:2000MAY01	3352	3405	forward 1	TM	N out
41	LI:1084246.1:2000MAY01	3409	3480	forward 1	TM	N out
41	LI:1084246.1:2000MAY01	3526	3609	forward 1	TM	N out
41	LI:1084246.1:2000MAY01	200	253	forward 2	TM	N in
41	LI:1084246.1:2000MAY01	2171	2254	forward 2	TM	N in
41	LI:1084246.1:2000MAY01	2654	2734	forward 2	TM	N in
41	LI:1084246.1:2000MAY01	3065	3142	forward 2	TM	N in
41	LI:1084246.1:2000MAY01	3284	3358	forward 2	TM	N in
41	LI:1084246.1:2000MAY01	3479	3553	forward 2	TM	N in
41	LI:1084246.1:2000MAY01	582	641	forward 3	TM	N out
41	LI:1084246.1:2000MAY01	2127	2213	forward 3	TM	N out
41	LI:1084246.1:2000MAY01	2457	2543	forward 3	TM	N out
41	LI:1084246.1:2000MAY01	2580	2666	forward 3	TM	N out
41	LI:1084246.1:2000MAY01	2751	2813	forward 3	TM	N out
41	LI:1084246.1:2000MAY01	2826	2888	forward 3	TM	N out
41	LI:1084246.1:2000MAY01	2961	3047	forward 3	TM	N out
41	LI:1084246.1:2000MAY01	3249	3335	forward 3	TM	N out
41	LI:1084246.1:2000MAY01	3429	3515	forward 3	TM	N out
42	LI:1165828.1:2000MAY01	61	147	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	244	312	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	454	510	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	3664	3750	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	3937	4023	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	4600	4653	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	4855	4941	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	5047	5133	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	5227	5298	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	5311	5388	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	5491	5577	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	5800	5871	forward 1	TM	N out
42	LI:1165828.1:2000MAY01	227	301	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	713	775	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	1769	1819	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	2759	2845	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	3869	3928	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	4688	4774	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	5048	5116	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	5531	5617	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	5816	5893	forward 2	TM	N in
42	LI:1165828.1:2000MAY01	39	113	forward 3	TM	N out
42	LI:1165828.1:2000MAY01	906	968	forward 3	TM	N out
42	LI:1165828.1:2000MAY01	1602	1688	forward 3	TM	N out
42	LI:1165828.1:2000MAY01	3471	3557	forward 3	TM	N out
42	LI:1165828.1:2000MAY01	3558	3608	forward 3	TM	N out
42	LI:1165828.1:2000MAY01	4203	4289	forward 3	TM	N out
42	LI:1165828.1:2000MAY01	4749	4835	forward 3	TM	N out

42	LI:1165828.1:2000MAY01	5625	5690	forward 3	TM	N out
42	LI:1165828.1:2000MAY01	5847	5918	forward 3	TM	N out
43	LI:007302.1:2000MAY01	346	426	forward 1	TM	N in
43	LI:007302.1:2000MAY01	2638	2721	forward 1	TM	N in
43	LI:007302.1:2000MAY01	59	145	forward 2	TM	N out
43	LI:007302.1:2000MAY01	653	718	forward 2	TM	N out
43	LI:007302.1:2000MAY01	1799	1885	forward 2	TM	N out
43	LI:007302.1:2000MAY01	321	407	forward 3	TM	N in
43	LI:007302.1:2000MAY01	480	566	forward 3	TM	N in
43	LI:007302.1:2000MAY01	645	704	forward 3	TM	N in
43	LI:007302.1:2000MAY01	807	890	forward 3	TM	N in
43	LI:007302.1:2000MAY01	1161	1223	forward 3	TM	N in
43	LI:007302.1:2000MAY01	1236	1298	forward 3	TM	N in
43	LI:007302.1:2000MAY01	1362	1448	forward 3	TM	N in
43	LI:007302.1:2000MAY01	1809	1868	forward 3	TM	N in
43	LI:007302.1:2000MAY01	1998	2084	forward 3	TM	N in
43	LI:007302.1:2000MAY01	2184	2234	forward 3	TM	N in
43	LI:007302.1:2000MAY01	2457	2540	forward 3	TM	N in
43	LI:007302.1:2000MAY01	2595	2681	forward 3	TM	N in
44	LI:236386.4:2000MAY01	3739	3792	forward 1	TM	N out
44	LI:236386.4:2000MAY01	53	118	forward 2	TM	N out
44	LI:236386.4:2000MAY01	218	304	forward 2	TM	N out
44	LI:236386.4:2000MAY01	3755	3823	forward 2	TM	N out
44	LI:236386.4:2000MAY01	2376	2435	forward 3	TM	N out
45	LI:252904.5:2000MAY01	494	550	forward 2	TM	N out
45	LI:252904.5:2000MAY01	300	374	forward 3	TM	N out

TABLE 4 (cont.)

4	1749048T6	1	388	1515410H1	1224	1442	4671595H1	2027	2277
5	996489H1	1	289	92056082	1221	1509	318659H1	2041	2291
5	996489R6	1	321	566614H1	1269	1530	4902185H1	2096	2297
5	6807726H1	9	414	4780315H1	1290	1553	92055975	2105	2298
5	91208184	74	603	1637781H1	1302	1454	1219763H1	2110	2288
5	91146490	110	406	1638827H1	1302	1455	1219763R6	2110	2290
5	1391557H1	145	273	1633937H1	1762	1969	1219763T6	2110	2251
5	2054016H1	155	406	6821354H1	1419	1971	1219763T1	2110	2250
5	3564377H1	213	498	1390745H1	1433	1557	581809H1	2110	2369
5	1389469H1	365	607	1932110H1	1712	1868	92788727	2119	2369
5	6178475H1	288	554	1932110F6	1713	1960	2753294H1	2255	2364
5	2490333H1	461	684	1850028H1	1728	1970	2055577R6	766	1137
5	1498011F6	497	816	386578H1	1753	2029	2055577T6	766	1096
5	1498011H1	497	735	1862471H1	1759	1870	91578280	767	1137
5	154577H1	512	727	4588296H1	1799	1890	94897043	769	1147
5	2439861H1	600	846	2028756H1	1816	1890	91897641	769	1137
5	6974170H1	655	1206	1988349T6	1824	2253	93004281	774	1138
5	5557446H1	723	990	1498011T6	1829	2254	6361438H2	776	1335
5	6821354J1	725	1336	6157225H1	1842	2101	1273945F1	790	1131
5	3801324H1	751	1035	521110H1	1850	1975	1273945H1	790	948
5	159257H1	753	952	6157733H1	1854	2051	2558966H1	791	1058
5	1562163H1	801	1030	4829815H1	1889	1962	92178992	831	1147
5	7161127H1	827	1358	4411517H1	1907	2157	91891843	842	1143
5	1840238H1	834	989	541981H1	1927	2155	91203333	844	1159
5	1892815H1	944	1194	4558860H1	1944	2106	91141073	845	1135
5	1883046H1	944	1185	1391452T6	1958	2260	91728655	851	1143
5	1391452H1	962	1131	2752758H1	1963	2239	4618322H1	860	1133
5	1391452F6	962	1223	1807380T6	1965	2250	93179203	882	1147
5	1680496H1	1117	1345	1807042F6	1970	2290	4164817H1	9	261
5	2132470R6	1120	1456	1807042H1	1970	2255	5851107H1	12	270
5	1265470H1	1149	1401	2311115H1	1992	2237	4938618H1	1	285
5	6804038H1	1164	1555	996489T6	1994	2332	2096384H1	13	274
5	3430883H1	1183	1428	6125387H1	2007	2356	4938518H1	1	184
5	2132470H1	1188	1456	4905520H1	2022	2280	6133436H1	6	304

TABLE 4 (cont.)

6	5218795H1	14	282	6	768284H1	670	900	6	5346772H1	29	227
6	3038155H1	6	294	6	92567185	671	1075	6	5346890H1	29	141
6	3088308H1	14	285	6	2522538H1	672	909	6	4151612H1	31	258
6	6821608H1	14	578	6	93446544	676	1136	6	92229063	27	371
6	5855412H1	14	297	6	4377572H1	680	948	6	3074071H1	31	308
6	2532161H1	6	258	6	94242762	685	1135	6	3717427H1	32	401
6	5999068H1	6	559	6	95444329	685	1147	6	2467222H1	32	258
6	95431297	7	324	6	94394905	687	1135	6	5687205H1	33	296
6	2715577H1	14	256	6	94891466	689	1136	6	92027890	31	188
6	3717266H1	6	312	6	4534880T1	604	1111	6	2864630H1	34	341
6	3088671H1	14	251	6	91422487	626	919	6	3837823H1	35	321
6	1690850T6	16	558	6	3213475H1	692	929	6	5978027H1	35	298
6	4978332H1	19	305	6	93674532	698	1150	6	3841249H1	35	236
6	2525160H1	368	619	6	93665343	700	1135	6	5780416H1	37	313
6	2811816H1	382	591	6	95365390	705	1135	6	4525495H1	38	294
6	5285481H1	381	530	6	3362353H1	708	848	6	2943180H1	35	281
6	91923667	380	575	6	93737258	707	1140	6	3159688H1	36	136
6	2724519H1	385	586	6	3801387H1	711	869	6	92156554	35	459
6	4403213H1	397	537	6	91277444	717	1135	6	5989823H1	38	334
6	2525196H1	368	597	6	6045963H1	722	1176	6	4525695H1	38	287
6	92111237	370	592	6	92236500	716	1139	6	774424H1	38	269
6	91155753	370	731	6	4024228H1	722	1008	6	4376239H1	38	242
6	92111348	371	598	6	94088002	718	1149	6	222536R1	19	533
6	93798474	371	588	6	3553263H1	754	969	6	4951501H2	19	325
6	92968466	372	670	6	92229274	762	1153	6	5986222H1	21	289
6	91874430	374	675	6	2055577H1	766	1031	6	4782312H1	19	258
6	93933996	376	589	6	5116334H1	19	290	6	222536H1	19	150
6	92567131	409	663	6	1546662H1	19	218	6	6152094H1	26	301
6	91422584	429	556	6	2275605H1	19	291	6	3365655H1	27	286
6	92157052	435	744	6	5968841H1	19	591	6	2098005H1	27	209
6	3092788H1	437	722	6	1902261H1	1	288	6	2874828H1	27	311
6	1650634F6	441	871	6	6728620H1	29	590	6	4748012H1	29	297
6	1831391H1	637	867	6	1690850F6	29	482	6	5122477H1	27	278
6	2173245H1	652	888	6	1690850H1	29	237	6	5516387H1	27	270

TABLE 4 (cont.)

6	5695974H1	27	203	6	5609131H1	123	365	6	95849856	504	739
6	4994832H1	36	185	6	93598018	135	590	6	6365612H1	519	816
6	91728758	40	325	6	93432506	136	593	6	5183801H1	525	789
6	5993725H1	40	342	6	95431490	144	323	6	3706413H1	529	812
6	5995510H1	40	330	6	91646810	57	324	6	4828553H1	532	762
6	94329715	40	406	6	92555607	156	500	6	2604912H1	539	791
6	2894305H1	47	310	6	91578371	53	198	6	92107086	553	977
6	2719394T6	303	625	6	92229126	158	593	6	95769539	555	733
6	95658221	327	736	6	93229125	173	598	6	5576107H1	559	800
6	5857676H1	296	564	6	93898868	173	593	6	91891969	565	972
6	5726056H2	297	676	6	94452177	180	323	6	3620132H1	31	324
6	2097760H1	300	546	6	93182012	205	593	6	4605074H1	598	846
6	2873090H1	329	605	6	790141R1	222	746	6	1650642F6	441	832
6	3136434H1	334	597	6	790141H1	222	456	6	3443641H1	484	742
6	91646811	339	596	6	3599189H1	229	519	6	93889543	490	917
6	2738075F6	321	767	6	92204943	229	593	6	93095491	492	586
6	2738075H1	321	564	6	3258218H1	232	529	6	2738075T6	494	1096
6	2719394F6	318	683	6	92355330	244	592	6	4534880H1	441	701
6	2719394H1	267	521	6	92882852	65	382	6	4277322H1	497	751
6	95527461	339	586	6	91950563	70	330	6	4989476F8	496	967
6	92437242	340	551	6	1548020H1	72	301	6	1650634H1	441	687
6	4724150H1	343	607	6	2823270H1	250	538	6	92575167	443	843
6	91312816	346	778	6	2873603H1	257	537	6	3718361H1	456	769
6	4787470H1	360	597	6	2755517H1	79	346	6	3267371H1	457	700
6	5003922H1	362	616	6	3718262H1	81	391	6	1902161H1	462	586
6	6156796H1	87	345	6	915491R6	260	597	6	5056004H1	465	746
6	2895320H1	43	273	6	915491H1	260	569	6	93751871	477	736
6	4665825H1	96	339	6	4979613H1	276	550	6	2997314H1	482	786
6	3232485H1	44	316	6	6821608J1	278	791	6	2996840H1	483	745
6	2399837H1	98	322	6	3246153H1	278	516	6	4276994H1	497	635
6	6904948H1	101	462	6	4008733H1	281	559	6	91923480	981	1130
6	6411519H1	45	554	6	4989076H1	497	752	6	6550669H1	1020	1619
6	035304H1	55	324	6	95850851	503	739	6	94083790	1388	1829
6	4573015H1	116	388	6	94738819	504	739	6	4700302H1	1388	1666

TABLE 4 (cont.)

6	93770915	1402	1832	12	975169T6	1112	1714	12	975169R6	855	1336
6	91224283	1032	1442	12	304276T6	1122	1713	12	4745248H1	1	241
6	92767747	1055	1135	12	6218188H1	1165	1678	13	7158869H1	7	479
6	2539090H1	1087	1334	12	5151940H1	1216	1440	13	3335250F6	34	398
6	1773532H1	1179	1391	12	975304T6	1231	1709	13	3335250H1	34	273
6	6045963J1	1211	1801	12	5531975T6	1266	1741	13	7077668H1	136	659
6	1650634T6	1270	1789	12	3577265H1	1286	1598	13	4318873H1	159	370
6	94373516	1308	1756	12	3016255H1	1291	1599	13	6992614H1	236	740
7	92524924	315	730	12	970343R6	1304	1757	13	753174H1	356	543
7	92161228	313	724	12	970343H1	1304	1606	13	7046749H1	453	1036
7	93802198	329	703	12	970343T6	1322	1714	13	6983112H1	621	891
7	93147794	231	688	12	3575519H1	1334	1616	13	9570318	630	905
7	92162211	119	550	12	5153116H1	1345	1469	13	5266308H1	632	788
7	2497157H1	78	310	12	988837H1	1422	1684	13	9778569	673	993
7	2854513H1	1	290	12	94088627	1503	1756	13	748982H1	672	901
8	1985316H1	1	269	12	6903302H1	1564	2110	13	744829R1	672	1226
8	1985316R6	1	310	12	975169H1	856	1057	13	744829H1	672	902
8	197972T6	43	445	12	92156118	1	475	13	9869715	672	1004
8	197972H1	43	274	12	975304H1	2	248	13	9565684	901	1080
8	197972R6	43	457	12	3403717H1	1	249	13	91025621	1027	1340
9	7197754H2	1	582	12	4042617H1	1	256	13	91059514	1027	1251
10	95810426	1	449	12	3042767H1	3	267	13	9714830	1108	1397
10	92219401	2	423	12	3042767F6	3	275	13	4311224H1	1203	1484
10	94329377	27	489	12	4854092H1	4	234	13	2292254R6	1398	1866
10	92537784	172	669	12	4743545H1	6	265	13	2292421R6	1398	1506
10	91376965	259	669	12	5856186H1	20	270	13	2291932H1	1398	1649
10	4983705H1	270	539	12	535036H1	27	246	13	530715H1	1423	1644
10	7269840H1	339	848	12	3960535H2	379	641	13	7090888H1	1520	1659
11	6453567H1	1	503	12	3960535F6	379	742	13	93086021	1518	1916
11	4052122H1	185	457	12	6216170H1	579	726	13	2291932T6	1559	2132
11	4052122F7	185	636	12	4456047H1	621	886	13	3335250T6	1562	2050
11	93897399	255	371	12	945050H1	762	1003	13	6841962H1	1748	2279
12	973628H1	996	1226	12	920681H1	855	1174	13	6855669H1	1881	2375
12	3014231H1	1097	1369	12	923436H1	855	1167	13	746910R6	1912	2375

TABLE 4 (cont.)

13	746910H1	1912	2143	14	g2930515	35	487	15	1670270F6	637	1077
13	746910T6	1913	2371	14	g4897951	44	477	15	g1921208	645	985
13	6844175H1	1941	2375	14	g09028H1	27	178	15	6523810H1	659	1052
13	2568562H1	1989	2222	14	g2782816	15	417	15	3499282H1	423	706
13	g4393425	1996	2415	14	g4326525	1	141	15	5852917H1	661	921
13	g4109519	2006	2375	14	g2525795	28	236	15	2247228H1	692	959
13	g2694947	2036	2375	15	g6450570	1077	1426	15	g851799	704	1030
13	g2703845	2040	2375	15	g6473965	97	472	15	4946358H1	711	972
13	g3884077	2042	2375	15	525308H1	117	324	15	5951390H1	729	954
13	g3278030	2045	2423	15	g2898932	121	456	15	6345162H1	792	1031
13	4705947H1	2104	2256	15	526619H1	129	370	15	3436737H1	794	1029
13	g714831	2110	2411	15	g2942591	134	271	15	g2264229	426	815
13	750787H1	2121	2365	15	2360586H1	145	399	15	3496822H1	430	703
13	667235H1	2126	2370	15	2211028H1	228	438	15	6321740H1	805	1031
13	g561290	2150	2375	15	987239R1	305	763	15	2112334H1	820	1080
13	g518739	2157	2375	15	987239H1	305	478	15	1007012H1	470	767
13	g3230679	2187	2375	15	1436565F1	354	824	15	2112334R6	820	1167
13	g717890	2318	2390	15	7161757H1	1	521	15	3215530H1	491	714
14	4145560H1	1	337	15	g4372435	23	212	15	3144904H1	873	1217
14	7182979H1	1	537	15	g5451540	23	516	15	g4073140	965	1444
14	g4929686	1	1581	15	g3884494	40	407	15	g4523268	970	1426
14	g1881193	113	359	15	g5545276	40	499	15	g5673767	972	1444
14	798770H1	206	449	15	2269559H1	44	305	15	2896020H1	496	741
14	g1198695	214	498	15	2269559R6	44	350	15	960106H1	971	1049
14	g1637735	380	642	15	g5152652	62	224	15	962045H1	971	1248
14	g2204679	39	511	15	3222733H1	86	303	15	5109444H1	498	723
14	5540595H1	1	195	15	1664718F6	91	349	15	g2070246	973	1335
14	g1970769	1	345	15	1664718H1	91	352	15	g2206523	973	1266
14	g1970753	1	325	15	g880746	97	278	15	g880857	501	815
14	g1971048	1	253	15	1436565H1	354	626	15	g5637498	978	1401
14	g1970777	1	223	15	2520441H1	360	641	15	g5449171	979	1439
14	g815792	8	284	15	3460138H1	393	644	15	3733518H1	980	1275
14	g1441646	3	303	15	6881873J1	142	680	15	g4763832	981	1444
14	g4372035	14	479	15	6881873H1	51	484	15	6807693H1	520	1140

TABLE 4 (cont.)

15	1968707R6	522	920	15	95904784	1090	1444	17	2158854T6	743	1154
15	95754504	985	1444	15	94852367	1094	1444	17	95543295	743	1201
15	95511006	992	1444	15	91443408	1101	1445	17	91385006	749	1056
15	6154958H1	991	1304	15	2124915H1	1117	1402	17	2158854H1	749	1012
15	92952676	993	1443	15	93412275	1126	1443	17	3973473H1	782	1055
15	1968707H1	522	727	15	95671642	1138	1407	17	3973473F8	783	1307
15	961381H1	997	1290	15	92056619	1211	1442	17	5629236F6	806	1288
15	6344762H1	534	632	15	94148637	1249	1426	17	3973473T8	883	1519
15	959580H1	997	1109	15	91921308	1253	1445	17	5629236H1	1062	1288
15	92209838	548	972	15	92952936	1256	1443	17	2777742H1	1069	1170
15	6856259H1	554	1067	15	92728303	1276	1446	17	2509368H1	1108	1343
15	2479125H1	565	804	15	94195307	1314	1444	17	2793074H2	1138	1253
15	4345262H1	577	856	15	92841540	1351	1445	17	2793074F6	1142	1253
15	959580R1	997	1433	16	1601184H1	304	515	17	2793074T6	1177	1260
15	94437873	998	1426	16	3540611H1	297	388	17	2364001H1	1404	1651
15	95661623	1002	1410	16	3111986H1	304	368	17	93898774	1582	1927
15	94332091	1006	1444	16	1673924H1	297	503	18	3224948H1	1	177
15	5031758H1	585	825	16	1569636H1	297	508	18	3695977H1	7	312
15	91320158	1008	1439	16	2696549F6	297	378	18	7006140H1	8	566
15	95391778	1012	1444	16	92219716	1	359	18	2794410H1	13	150
15	95933236	1012	1444	16	92898608	1	211	18	6460326H1	40	396
15	92901335	1014	1408	16	6755069H1	1	654	18	6787346H1	51	555
15	91940416	1015	1444	16	3539560H1	303	476	18	3403667H1	53	289
15	95113563	1021	1444	16	1515102H1	297	466	18	3725949H1	56	297
15	2517547H1	1043	1277	16	1572728H1	297	492	18	2830626H1	61	333
15	95451354	1053	1284	16	1347783H1	309	435	18	91646403	62	445
15	92220466	1062	1408	16	1691349H1	297	436	18	2830626F6	61	581
15	92952784	1064	1440	16	3686316H1	304	498	18	6784569H2	61	591
15	3329431H1	607	885	17	4563458H1	1	197	18	5959276H1	74	534
15	5271370H1	618	855	17	4381069H1	15	261	18	6804522J1	100	522
15	1670270H1	637	862	17	6205262H1	107	542	18	3697994H1	118	356
15	91367649	1071	1444	17	6202507H1	412	921	18	581170H1	133	223
15	93751105	1073	1444	17	4620133F6	603	940	18	5610623H1	133	408
15	91367704	1083	1437	17	4620133H1	603	851	18	2770068H1	157	405

TABLE 4 (cont.)

18	7165406H1	159	535	19	1651460H1	83	301	23	2586194T6	1977	2477
18	6702265H1	312	825	19	6264819H1	186	461	23	6479875H1	1990	2477
18	7037116H1	372	699	19	4753777H1	214	338	23	2856722H1	2000	2267
18	6531787H1	511	922	19	2331424R6	333	638	23	1298131T6	2038	2472
18	1214116H1	519	662	19	2331424H1	333	560	23	1298131H1	2038	2291
18	6804522H1	637	1171	19	3398569H1	339	582	23	1298131F1	2038	2276
18	7218713H1	677	1237	19	2435387H1	342	570	23	1298131F6	2038	2516
18	3557937H1	687	987	19	506031H1	351	527	23	2300965T6	2040	2476
18	6455665H1	825	1420	19	6118353H1	362	469	23	94075934	2067	2517
18	6701662H1	821	1297	19	609565H1	377	628	23	93415730	2098	2518
18	6523244H1	847	1324	19	2873416H1	397	540	23	92139392	2111	2489
18	4004887H1	926	1204	20	2583409H1	204	430	23	94735514	2111	2514
18	4876106H1	945	1182	20	92823866	1	383	23	94261130	2111	2518
18	4067628F7	1082	1353	20	3488619H1	1	280	23	94665764	2111	2513
18	6932868H1	1082	1543	20	5633561F6	207	798	23	3483466H1	2111	2363
18	3191237H1	1103	1414	20	5633561H1	207	465	23	953666013	2119	2512
18	7088151H1	1126	1596	21	94690049	1	195	23	94599402	2126	2517
18	2818868H1	1173	1275	21	1398471F6	1	410	23	4096757H1	2144	2441
18	5582555H1	1189	1439	21	1399832H1	1	227	23	2254547H1	2151	2380
18	5582587H1	1188	1442	21	2694772H1	126	337	23	91692867	2185	2513
18	94893540	1220	1631	21	2694772F6	125	338	23	91157366	2204	2513
18	4442851H1	1276	1544	21	1398471H1	1	238	23	91128313	2281	2514
18	3022715H1	1325	1618	22	5286647F9	1	615	23	92524394	2295	2514
18	3780205H1	1349	1644	22	3808866F8	5	457	23	91227222	2316	2513
18	91947313	1365	1595	22	7264977H1	17	605	23	5913552F6	2405	2537
18	2996242H1	1384	1678	22	4760775F6	38	607	23	2265479H1	2413	2516
18	3052021H1	1414	1704	22	5286647T9	242	819	23	5913552H1	2416	2504
18	93095711	1478	1951	22	5286647T8	506	825	23	5643316H1	1884	2089
18	3927236H1	1596	1856	22	5286647F8	5	552	23	5794438H1	1854	2089
18	2769806H1	1625	1854	22	628206T7	1954	2472	23	5791230H1	1854	2089
18	5866616H1	1749	1842	23	277808H1	1974	2264	23	5791375H1	1854	2089
18	3730361H1	1767	1870	23	278730H1	1976	2309	23	856338H1	1129	1361
18	7169445H1	1	343	23	275057H1	1976	2160	23	3280567H1	1148	1399
19	6546889H1	1	339	23	275257H1	1976	2193	23	6551617H1	1183	1732

TABLE 4 (cont.)

23	6552317H1	1183	1762	23	5792646H1	1854	2162	24	4717574T6	1186	1635
23	6751972H1	1191	1762	23	5792285H1	1854	2089	24	1476570F6	1188	1656
23	5759260H1	1193	1468	23	5793871H1	1854	2089	24	1476571F6	1188	1532
23	4190084H1	1198	1471	23	4358460H1	1059	1303	24	1476570H1	1188	1394
23	6136366H1	1270	1571	23	g2142328	1	284	24	g614326	1200	1657
23	4205570H1	1301	1533	23	5662770H1	1	178	24	1476571T6	1206	1619
23	3354295H1	1305	1539	23	7004664H1	142	653	24	g4152280	1219	1388
23	4303867H1	1317	1502	23	g1692967	194	528	24	g4598685	1229	1657
23	628206H1	1382	1615	23	265733H1	224	448	24	g314775	1244	1656
23	628206R7	1382	1793	23	6406758H1	542	995	24	2153570H1	1241	1515
23	4337705H1	1443	1782	23	6259622H1	667	954	24	4492503H1	1247	1657
23	2881556H1	1467	1726	23	g1628822	753	1138	24	g615988	1254	1656
23	6875744H1	1469	2058	23	2587028H1	876	1152	24	g775420	1264	1670
23	5677351H1	1496	1741	23	3331574H1	913	1177	24	5659105H1	1264	1344
23	2772870H1	1505	1749	23	705890H1	915	1149	24	g4617815	1272	1663
23	1212235R6	1541	1990	23	705979H1	915	1181	24	g5511164	1274	1656
23	1212235H1	1541	1815	23	4114902H1	922	1125	24	g3649444	1275	1658
23	g1646733	1551	1869	23	2889650H1	968	1241	24	g314750	1287	1656
23	2297674H2	1562	1829	23	6507226H1	1058	1499	24	004952H1	1164	1423
23	2586194H1	1590	1839	23	6258095H1	1059	1340	24	1476570T6	1171	1617
23	2586194F6	1590	2059	24	g314920	1324	1655	24	4705993T9	1106	1554
23	2403715H1	1606	1845	24	g615297	1324	1656	24	1270695T6	1177	1617
23	6859287H1	1655	2089	24	g517687	1324	1655	24	2416693T6	1090	1611
23	5091604H1	1689	1969	24	g615578	1370	1656	24	748579R1	1076	1656
23	2736946H1	1689	1940	24	g614283	1374	1656	24	859218H1	1007	1221
23	2823882H1	1714	2005	24	1456735T6	1422	1622	24	g6086997	903	1254
23	2821255H1	1714	2025	24	g4328099	1446	1662	24	533539T6	909	1226
23	573737H1	1740	1857	24	g614262	1449	1656	24	5371992T9	942	1580
23	6350742H1	1769	2058	24	g4152278	1455	1656	24	g314842	948	1254
23	2300965H1	1775	2006	24	g562532	1461	1656	24	g683067	970	1254
23	2300965R6	1775	2170	24	g671207	1462	1656	24	7290682H1	978	1513
23	439474H1	1808	2043	24	5945223H1	1578	1660	24	009349H1	761	1103
23	5686929H1	1843	2106	24	g2985356	1621	1848	24	6888770H1	772	1287
23	5794171H1	1854	2162	24	5498383R6	1236	1619	24	6866213H1	772	1377

TABLE 4 (cont.)

24	4943311T6	785	1231	24	1456735F6	189	605	24	6768978J1	33	631
24	7292792H1	793	1368	24	6721132H1	193	579	24	92003419	45	421
24	91192539	802	1254	24	4203426H1	212	337	24	91551472	61	213
24	94223790	815	1254	24	1992224H1	206	475	24	6147606H1	71	625
24	6717166H1	821	1283	24	7259028H1	204	579	24	9615579	115	462
24	93331126	836	1256	24	9766593	289	587	24	9389770	122	510
24	5310872H1	838	1064	24	7058996H1	305	886	24	6888770J1	153	753
24	5267191H1	858	1118	24	4092963H1	327	609	24	9615989	174	503
24	4940779H1	878	1150	24	9614162	336	605	24	4943311H1	175	458
24	1270258H1	880	1118	24	9677813	336	565	24	4943311F6	175	595
24	9794503	887	1267	24	6985794H1	332	788	24	6818987H1	197	267
24	9816007	884	1243	24	4338771H1	359	628	24	1853628H1	181	421
24	9901436	892	1254	24	9708822	393	694	24	1456735H1	208	332
24	6869327H1	724	1228	24	9764692	395	736	24	5920291H1	208	267
24	6855475H1	1045	1242	24	9816062	378	790	24	7290834H1	187	505
24	1270292T6	1048	1610	24	3864471H1	374	591	24	6818987J1	33	250
24	9822109	1058	1267	24	6990907H1	383	921	24	6818431J1	33	570
24	748579H1	1064	1304	24	91627181	208	330	24	92003054	31	344
24	859218R6	1007	1446	24	5311056H1	591	753	24	6770575J1	35	555
24	9567610	1012	1254	24	5907142H1	659	938	24	91192915	25	170
24	859218R1	1007	1527	24	5924427H1	681	971	24	91978747	1	307
24	859218T6	1046	1617	24	2707020H1	557	850	24	95553287	1	315
24	1270695F6	541	829	24	5205391H1	565	805	24	6989857H1	1	436
24	1270695H1	541	773	24	5498383H1	573	811	24	6955370H1	22	540
24	7067123H1	525	1069	24	5498383F6	573	1055	24	94390046	24	500
24	6448066H1	400	951	24	94152281	207	277	24	94534562	24	504
24	9691925	443	755	24	7290347H1	188	672	25	7177245H2	1	455
24	533539R6	431	951	24	1265660F1	176	785	25	93015541	154	2103
24	533539H1	427	622	24	1265660H1	181	469	25	91864084	221	2759
24	5379139H1	434	679	24	3944530H1	184	461	25	9694473	448	790
24	6868778H1	494	1123	24	9677040	204	322	25	9710265	448	736
24	5674272H1	391	645	24	91950097	237	294	25	9900615	470	914
24	6120160H1	386	785	24	6773005J1	33	637	25	9900616	469	798
24	6866026H1	381	974	24	6765966J1	33	606	25	4720263F6	580	1018

TABLE 4 (cont.)

25	4720263H1	582	820	26	94332214	139	571	26	70880461V1	839	1433
25	96142053	718	1125	26	5204807H1	152	395	26	4761241H1	884	1159
25	93095833	754	886	26	7066891H1	196	711	26	4761249H1	885	1169
25	7213511H1	762	1242	26	70882460V1	324	844	26	9901677	927	1310
25	9705775	879	1219	26	6559677H1	357	941	26	9946847	928	1263
25	91275210	960	1173	26	70881844V1	392	965	26	9953373	928	1130
25	6551517H1	1098	1692	26	70879312V1	427	993	26	70818743V1	944	1123
25	096164H1	1151	1387	26	7239855H1	468	1020	26	70879516V1	955	1615
25	5451192H1	1222	1451	26	9830101	474	849	26	70882124V1	977	1488
25	1308461F6	1230	1655	26	9889334	474	843	26	70881307V1	1002	1476
25	1308461H1	1230	1360	26	6559338H1	490	770	26	70879227V1	1036	1255
25	385195H1	1364	1640	26	6721187H1	534	1104	26	3803043H1	1037	1326
25	3415579H1	1387	1650	26	70882570V1	535	1028	26	3013311H1	1056	1341
25	91191407	1788	1959	26	5780844H1	542	821	26	6883273J1	1061	1663
25	4765883H1	2166	2412	26	70882690V1	558	1104	26	3457862H1	1084	1327
25	4760585H1	2225	2489	26	5780844F6	565	1096	26	9316332	1120	1339
25	1308461T6	2272	2720	26	2154958H1	565	667	26	70880271V1	1130	1719
25	658904H1	2278	2532	26	70880555V1	597	1241	26	70882630V1	1138	1274
25	92987356	2301	2759	26	70888508V1	603	936	26	1391847F6	1155	1647
25	92987355	2304	2759	26	1394886F6	630	1075	26	1391847H1	1155	1407
25	4720263T6	2360	2746	26	1394886H1	630	888	26	5292536H2	1163	1394
25	1308461R1	2486	2759	26	1392996H1	630	891	26	70879978V1	1205	1732
25	93887078	2491	2762	26	671307H1	655	933	26	2453848H1	1218	1444
25	9824280	2507	2769	26	1270677H1	663	905	26	1703631H1	1230	1354
26	3315579H1	1	246	26	6560774H1	677	1208	26	70879064V1	1237	1843
26	2564790H1	4	144	26	70885252V1	693	934	26	70881312V1	1275	1788
26	7037134H1	17	591	26	7289657H1	729	1231	26	5365719H1	1276	1432
26	92214897	120	460	26	92215028	736	1137	26	4753468H1	1281	1550
26	70879775V1	123	576	26	6945491H1	746	1269	26	1966807H1	1286	1555
26	70882313V1	123	561	26	70887853V1	770	894	26	70881555V1	1332	1998
26	70881021V1	123	654	26	70881667V1	773	1363	26	70818654V1	1368	1926
26	70881583V1	123	700	26	6986634H1	816	1297	26	1350180H1	1376	1646
26	3539234F6	123	536	26	1374120H1	825	961	26	70879359V1	1382	1871
26	3539234H1	123	348	26	70882560V1	830	1440	26	6020187H1	1410	2009

TABLE 4 (cont.)

26	70881816V1	1422	2015	26	g2875209	1886	2068	28	g1406097	2583	3005
26	3027682T6	1438	2026	26	70879855V1	1958	2305	28	g1406068	2588	3005
26	1394886T6	1450	2027	26	70882152V1	2018	2288	28	g2703843	2588	3002
26	2301449H1	1455	1541	26	6554433H1	2886	3287	28	g1156665	2602	2792
26	70885937V1	1452	1711	26	g5863770	4005	4350	28	852284H1	2611	2841
26	1391847T6	1461	2030	27	5911592T6	1	523	28	852284R6	2613	2844
26	3447875H2	1468	1723	27	5911592H1	1	290	28	3477842H1	2612	2706
26	4030281T8	1479	1804	27	5911592T8	1	473	28	g2714143	2634	3005
26	70881238V1	1492	2020	27	5911592F8	1	569	28	2362491H1	2657	2912
26	70880651V1	1539	2110	27	5911592T9	1	473	28	g1635193	2665	2792
26	4061612H1	1580	1860	27	5911592F6	1	565	28	552048H1	2670	2921
26	g5863332	1584	2067	28	g1187505	3265	3546	28	5912223H1	2682	2748
26	g5111312	1587	2067	28	g1128275	3293	3495	28	g3412761	2692	3005
26	2877413H1	1607	1908	28	g1507227	3296	3546	28	3492839H1	2695	2980
26	2877413F6	1607	2002	28	g899953	3306	3566	28	g1507002	2710	2916
26	g3281621	1609	2068	28	g1080424	3307	3542	28	5041915H1	2710	2899
26	70818645V1	1622	2077	28	g62712H1	3307	3546	28	643875H1	2715	2976
26	g4535191	1624	2068	28	1923976H1	3314	3512	28	2531919H1	2731	2885
26	g3426844	1626	2067	28	g2159328	3320	3551	28	g6138438	2732	3005
26	g2322267	1644	2068	28	g735553	3320	3545	28	4623249H1	2732	3002
26	g6196543	1654	1928	28	g5913481	3323	3554	28	2890187H1	2734	2998
26	g3134994	1660	2074	28	g3896209	3322	3546	28	g1670564	2741	3248
26	g2874749	1663	2068	28	g795225	3331	3556	28	1850848H1	2754	3062
26	2877413T6	1681	2018	28	g2185988	2435	2887	28	g3659213	2760	3290
26	g830043	1717	2080	28	4716403H1	2441	2550	28	956983H1	2762	3049
26	g946801	1740	2052	28	112524H1	2441	2661	28	019839H1	2786	3082
26	3539234T6	1764	2255	28	g6142912	2452	3005	28	3813377H1	2823	3095
26	g889242	1768	2079	28	4582601H1	2503	2780	28	131061H1	2831	2930
26	g3178069	1789	2068	28	4733207H1	2515	2810	28	7054832H1	2837	3406
26	4000739H1	1795	2068	28	g1320604	2527	3046	28	804820H1	2856	3090
26	g1372960	1812	4328	28	3254646H1	2529	2781	28	1842462H1	2878	3146
26	g3094856	1852	2068	28	2273834H1	2542	2797	28	4792127H1	2882	3145
26	g5528202	1869	2072	28	2688820H1	2567	2829	28	1494563H1	2882	3121
26	70887416V1	1885	2293	28	3449902H1	2576	2832	28	1753953H1	2883	3125

TABLE 4 (cont.)

28	1755130H1	2883	3092	93897396	3097	3546	28	g3897396	3097	3546	28	3256027H1	3561	3626
28	3941233H1	2902	3198	612568H1	3098	3355	28	612568H1	3098	3355	28	3256027R6	3561	3626
28	2116653H1	2902	3193	93278888	3101	3551	28	93278888	3101	3551	28	91959467	1	63
28	2404516H1	2914	3172	92899655	3101	3544	28	92899655	3101	3544	28	076140H1	1	230
28	4524703H1	2917	3027	93744156	3103	3546	28	93744156	3103	3546	28	3400145H1	42	272
28	91617791	2942	3256	92185814	3109	3552	28	92185814	3109	3552	28	7166689H1	77	373
28	4407776H1	2934	3211	6715165H1	3111	3548	28	6715165H1	3111	3548	28	5513977H1	89	336
28	5186425H1	2942	3195	4864862H1	3117	3405	28	4864862H1	3117	3405	28	4970421H1	89	348
28	2904404H1	2942	3200	1968272R6	3132	3548	28	1968272R6	3132	3548	28	96300096	153	586
28	3144463H1	2943	3262	1968272T6	3132	3501	28	1968272T6	3132	3501	28	5335382H1	256	490
28	2359103T6	2953	3498	1968272H1	3132	3401	28	1968272H1	3132	3401	28	5335373H1	257	488
28	4652661H1	2961	3062	1492449H1	3133	3347	28	1492449H1	3133	3347	28	1437260F1	264	814
28	2955930H1	2977	3261	94648047	3136	3547	28	94648047	3136	3547	28	1437260F6	264	658
28	3115379T6	2982	3507	94438953	3138	3539	28	94438953	3138	3539	28	1437260H1	264	533
28	852284T6	2987	3507	92751861	3143	3349	28	92751861	3143	3349	28	5373320H1	290	505
28	1661229T6	2988	3505	9572806	3150	3528	28	9572806	3150	3528	28	6485087H1	404	923
28	3822074H1	2994	3275	9672266	3150	3466	28	9672266	3150	3466	28	4181761H1	414	498
28	4229083H1	2994	3263	9879603	3150	3402	28	9879603	3150	3402	28	5026859H1	610	693
28	3842223H1	2994	3234	9876360	3151	3531	28	9876360	3151	3531	28	3230444H1	616	763
28	3607528H1	2996	3166	9830456	3151	3412	28	9830456	3151	3412	28	2134545F6	767	1341
28	91080514	2999	3320	321502H1	3151	3397	28	321502H1	3151	3397	28	2134545H1	767	1022
28	1661229F6	3011	3447	337082H1	3151	3381	28	337082H1	3151	3381	28	265345H1	787	970
28	1661225H1	3011	3202	94891955	3153	3546	28	94891955	3153	3546	28	1437260T6	791	1270
28	008660H1	3047	3339	95658866	3163	3547	28	95658866	3163	3547	28	3792193H1	878	1098
28	2321285H1	3047	3289	3023052H1	3163	3443	28	3023052H1	3163	3443	28	7260531H1	921	1369
28	92106118	3064	3549	93884073	3170	3546	28	93884073	3170	3546	28	6986910H1	986	1376
28	868783H1	3065	3326	95325327	3330	3546	28	95325327	3330	3546	28	4447338H1	1008	1169
28	95176750	3073	3550	91140821	3332	3546	28	91140821	3332	3546	28	6494154R9	1031	1550
28	92899654	3073	3546	2893166T6	3341	3509	28	2893166T6	3341	3509	28	4832434H1	1037	1301
28	94762266	3073	3549	92204552	3349	3551	28	92204552	3349	3551	28	2633783H1	1037	1287
28	6307419H1	3080	3547	91670543	3357	3546	28	91670543	3357	3546	28	91984595	1056	1311
28	94269311	3078	3549	91190688	3385	3493	28	91190688	3385	3493	28	2359103R6	1060	1504
28	94075892	3078	3546	2552971H1	3401	3550	28	2552971H1	3401	3550	28	2359103H1	1060	1314
28	93740929	3094	3555	5907555H1	3487	3644	28	5907555H1	3487	3644	28	5215646H1	1093	1294

TABLE 4 (cont.)

28	425878H1	1096	1306	28	5845309H1	1816	1911	28	675502H1	2177	2446
28	288744H1	1164	1454	28	3806331F6	1820	1915	28	3903169H1	2207	2492
28	6531566H1	1238	1809	28	6736585H1	1754	1823	28	3245445H1	2240	2454
28	7191895H2	1327	1801	28	487499H1	1809	2069	28	9827828	2241	2461
28	288744F1	1349	1793	28	5914004H1	1846	2125	28	4833872H1	2258	2461
28	96140330	1356	1781	28	6408595H1	1852	2414	28	91273258	2260	2749
28	96505751	1406	1704	28	91523070	1921	2355	28	4833888H1	2262	2538
28	7029795H1	1414	2023	28	9900055	1922	2243	28	91799398	2268	2712
28	5641161H1	1506	1745	28	5019562H1	1931	2111	28	91406166	2268	2643
28	4061776T6	1508	1704	28	92103229	1933	2320	28	91406194	2269	2631
28	4061776F6	1515	1875	28	92204602	1939	2229	28	5185315H1	2285	2542
28	4061776H1	1516	1704	28	2501393H1	1944	2111	28	2082955H1	2295	2598
28	92106291	1517	1824	28	91281535	1964	2431	28	6341726H1	2316	2810
28	91880733	1522	1738	28	9735660	1994	2170	28	594752H1	2355	2602
28	91441510	1522	1904	28	2813574H1	2020	2303	28	9942919	2366	2583
28	767028H1	1524	1704	28	2170420H1	2030	2277	28	7249143H1	2381	2613
28	4177249H1	1546	1816	28	3718831H1	2031	2320	28	91921577	2394	2864
28	9823676	1505	1807	28	4062530H1	2048	2342	28	2896518H1	2411	2658
28	93230537	1592	2020	28	91190010	2075	2225	28	91987258	2429	2848
28	3115379H1	1620	1700	28	4151403H1	2147	2211	28	92161140	2435	2928
28	93840134	1582	1751	28	962698R2	2147	2672	28	93430807	3172	3546
28	109465H1	1628	1784	28	96301662	2147	2523	28	6737055H1	3179	3546
28	951131H1	1599	1811	28	3716245H1	2147	2399	28	2118476H1	3179	3436
28	2431313H1	1621	1683	28	3090607H1	2147	2385	28	5511767H1	3182	3389
28	2134834H1	1679	1912	28	962698H1	2147	2367	28	2782179F6	3201	3588
28	3811087H1	1700	1965	28	2858893H1	2147	2351	28	2782195H1	3201	3468
28	3661827H1	1726	1863	28	5586368H1	2147	2348	28	3526177H1	3202	3479
28	3729456T6	1688	1751	28	2571180H1	2147	2332	28	94990081	3213	3546
28	93755762	1742	1806	28	4333921H1	2147	2350	28	3734501H1	3227	3528
28	2292441H1	1742	1982	28	6219737H1	2147	2352	28	93043004	3236	3546
28	2293368H1	1745	1970	28	640836H1	2147	2227	28	91200843	3238	3546
28	91939049	1757	2016	28	91196242	2168	2576	28	91243436	3243	3545
28	717351H1	1759	1999	28	91190446	2168	2444	28	896988R1	3244	3546
28	9827645	1759	1975	28	91832964	2172	2494	28	896988H1	3245	3472

TABLE 4 (cont.)

28	g4330537	3255	3553	29	6929893H1	1484	1917	29	672763T6	2553	2659
28	g883772	3264	3559	29	160750H1	1667	1758	30	6572615H1	1	572
29	2837088H1	1	79	29	6201684H1	1683	2203	31	6991082H1	1	215
29	382301H1	11	278	29	2684917H1	1733	1978	31	g4195018	4	167
29	382301R6	11	248	29	3898190H1	1945	2241	31	g5444909	10	139
29	381716R1	11	488	29	5983503T8	1966	2626	31	g5765521	10	480
29	6853095H1	18	566	29	5952437H1	1989	2278	31	g4736683	10	469
29	3296833H1	24	294	29	3637810T9	2048	2597	31	g5110384	10	474
29	492559R1	36	582	29	3151953H1	2057	2297	31	g5744052	26	461
29	492554H1	36	280	29	6357422H1	2085	2377	31	7181281H1	31	570
29	6710369H1	84	612	29	382301T6	2092	2657	31	3801178H1	71	269
29	g770845	381	657	29	2498615F6	2107	2537	31	6606927H1	91	475
29	6710369J1	556	1057	29	2498615H1	2107	2341	31	5725556H1	402	875
29	6866894H1	767	1363	29	492559F1	2134	2696	31	6459774H1	790	1082
29	2045879F6	814	1144	29	381716F1	2136	2696	32	g3744008	2026	2487
29	2045879H1	814	1085	29	4701147H1	2164	2436	32	g3843455	2032	2490
29	g677645	874	1174	29	g5435909	2244	2701	32	g4334045	2035	2487
29	g570913	874	1259	29	7067611H1	2285	2803	32	1295257F1	1686	2102
29	g878213	875	1218	29	g2563607	2313	2696	32	1295579H1	1686	1944
29	3637810H1	925	1212	29	1889064H1	2331	2615	32	1295615H1	1686	1932
29	3637810F8	926	1371	29	5762206H1	2333	2712	32	1295257H1	1686	1914
29	5516287H1	958	1216	29	2400488H1	2334	2587	32	g1382767	1690	2060
29	310657H1	1003	1205	29	g817549	2339	2706	32	3009590H1	1709	2019
29	054856H1	1048	1292	29	g566965	2376	2696	32	g1327091	1710	2099
29	2676843H1	1123	1318	29	g1894154	2387	2696	32	1496765H1	1766	2002
29	2865460H1	1206	1437	29	g869609	2428	2705	32	4604681H1	1772	2045
29	5983503F8	1245	1610	29	g4291206	2430	2805	32	1596414H1	1772	1993
29	5983503H1	1247	1545	29	g646309	2432	2696	32	6413696H1	1785	2102
29	6540006H1	1281	1578	29	7214349H1	2497	2879	32	4534504H1	1813	2098
29	3903656H1	1312	1525	29	3249908H1	2502	2799	32	71227864V1	1847	2362
29	2554026H1	1346	1615	29	672907H1	2553	2696	32	2210129H1	1863	2101
29	g1894266	1350	1824	29	672763R6	2553	2696	32	1447743H1	1866	2103
29	7039759H1	1414	1941	29	672763H1	2553	2696	32	70861405V1	1894	2228
29	6481201H1	1452	1566	29	672696H1	2553	2696	32	70861649V1	1895	2495

TABLE 4 (cont.)

32	6846658H1	1908	2107	32	g2657562	2083	2489	32	70793876V1	950	1625
32	4534504T1	1907	2456	32	g5631144	2082	2483	32	71228166V1	983	1533
32	4198839H1	1920	2101	32	70861820V1	2094	2484	32	3809253H1	1007	1304
32	1738412T6	1927	2437	32	g4534051	2102	2483	32	1617271H1	1066	1279
32	1737079H1	1932	2060	32	g653111	2102	2485	32	2863928H1	1081	1360
32	1738412H1	1932	2053	32	g2741121	2113	2483	32	3234412H1	1087	1342
32	g776871	1597	1846	32	g3900137	2112	2489	32	70861726V1	1187	1695
32	2477944H1	1596	1816	32	g4987139	2120	2488	32	6999153H1	1207	1857
32	4250426H1	1611	1861	32	g1327037	2121	2495	32	71228213V1	1213	1797
32	2920084H1	1623	1883	32	g3750723	2123	2491	32	754707H1	1226	1478
32	70862374V1	1651	2227	32	1712684T6	2129	2444	32	70860887V1	1228	1790
32	3602331H1	1634	1931	32	5900418H1	2135	2462	32	71228275V1	1235	1732
32	6868176H1	1636	2103	32	5900174H1	2134	2421	32	70861627V1	1248	1846
32	4675720H1	1639	1854	32	6811079J1	1	540	32	3807022H1	1269	1442
32	1561242F6	1658	2077	32	60205155U1	12	248	32	2950342H1	1277	1544
32	1561242H1	1658	1879	32	6886573J1	39	560	32	2952767H1	1277	1536
32	g1501696	1667	1973	32	6886573H1	111	596	32	71227990V1	1298	1936
32	g760301	1677	1915	32	6811079H1	185	755	32	71228136V1	1303	1784
32	g3278095	2137	2493	32	1453667F1	262	721	32	71227553V1	1310	1757
32	5900945H1	2134	2423	32	1453667H1	262	526	32	70861671V1	1323	1920
32	g6138412	2137	2496	32	1453667F6	262	546	32	70794764V1	1336	1702
32	g4330820	2257	2483	32	70818382V1	262	390	32	3140045H1	1338	1625
32	g1988368	2268	2493	32	3747731H1	327	524	32	70864551V1	1353	1859
32	g3843397	2293	2490	32	973584H1	340	620	32	6210975H1	1357	1668
32	g3920269	2298	2486	32	4043303H1	376	512	32	g653225	1358	1597
32	4069039H1	2330	2505	32	857173H1	550	783	32	70862132V1	1378	2033
32	g6475333	2337	2487	32	6258691H1	598	695	32	4701559H1	1384	1655
32	312604H1	2371	2483	32	3408105H1	614	890	32	7159432H1	1388	1905
32	313091H1	2371	2483	32	6606911H1	661	1207	32	2109285H1	1398	1660
32	313091R6	2371	2483	32	4579377H1	669	938	32	70864775V1	1403	2064
32	311262H1	2371	2483	32	3232119H1	686	966	32	70863822V1	1406	2038
32	313091T6	2371	2444	32	4142126H1	717	926	32	7343876H1	1408	2057
32	g794966	2420	2488	32	g3405461	764	1127	32	1679948H1	1413	1645
32	5585271H1	2056	2170	32	70818359V1	915	1488	32	6210776H1	1438	1754

TABLE 4 (cont.)

32	3866536H1	1442	1582	32	g2139296	2137	2481	33	70917213V1	1926	2485
32	1712684F6	1443	1998	32	g1382788	2139	2484	33	1420994F6	1937	2433
32	1712684H1	1443	1662	32	1453667T6	2144	2442	33	2661285H1	1939	2207
32	g758871	1444	1620	32	g1501595	2147	2497	33	1690542H1	1958	2166
32	4426067H1	1466	1711	32	4401648H1	2175	2229	33	4044243H1	1965	2248
32	70795476V1	1472	1640	32	g760248	2190	2477	33	g841565	1971	2225
32	5599333H1	1493	1727	32	g3249913	2212	2489	33	4633881H1	2015	2270
32	70797042V1	1502	1640	32	g852879	2240	2477	33	587465H1	2060	2372
32	6835201H1	1538	2080	32	g4509561	2255	2483	33	756115R1	2094	2667
32	70863377V1	1540	1989	32	6532986H1	2257	2483	33	756115H1	2094	2348
32	6844445H1	1560	2067	33	g779790	1220	1417	33	3465750H1	2098	2249
32	5155068H1	1560	1818	33	6117455H1	1343	1638	33	71274483V1	2113	2783
32	g852973	1573	1906	33	4733091H1	1405	1663	33	6609076T2	2142	2819
32	g851729	1573	1861	33	2614356H1	1420	1671	33	71272794V1	2155	2817
32	g793415	1573	1781	33	2614355H1	1420	1569	33	3927045H1	2179	2474
32	6124452H1	1584	2062	33	1340369F6	1474	1756	33	3928245H1	2179	2470
32	g788826	1597	1904	33	1340369H1	1474	1661	33	3674253T9	2226	2768
32	2130055H1	2435	2493	33	70920240V1	1488	2070	33	2658953H1	2242	2504
32	4238420H1	1936	2082	33	757294H1	1551	1778	33	70920349V1	2261	2805
32	g2138791	1962	2385	33	2658667H1	1624	1866	33	4735215H1	2262	2523
32	4351833H1	1979	2053	33	2771444H1	1749	1989	33	1294470T6	2271	2833
32	71225822V1	1984	2102	33	1312886F6	1751	2202	33	2791572T6	2319	2835
32	71225814V1	1981	2104	33	1312886H1	1751	1949	33	5058201H2	2320	2433
32	g4390230	2003	2493	33	2308711H1	1755	1965	33	1420994T6	2346	2837
32	g4738336	2009	2484	33	3519383H1	1755	1939	33	1312886T6	2355	2836
32	g4902383	2012	2483	33	2306567H1	1756	1936	33	1430732H1	2353	2616
32	71228259V1	2018	2229	33	1304465H1	1765	2003	33	2791668T6	2357	2837
32	g4436056	2019	2491	33	5172484H1	1779	2028	33	2791572F6	645	894
32	71227844V1	2018	2304	33	4172237H1	1810	2077	33	6828289J1	663	1310
32	g6037828	2021	2487	33	2877775H1	1839	2116	33	70919806V1	671	1312
32	g3740552	2022	2489	33	869079H1	1839	2071	33	124724H1	738	882
32	g3418190	2137	2493	33	3939024H1	1856	2135	33	g652789	805	1068
32	g3213525	2137	2487	33	71273416V1	1860	2454	33	2251573H1	819	1077
32	1561242T6	2136	2435	33	1420994H1	1918	2156	33	71274255V1	948	1609

TABLE 4 (cont.)

33	70920002V1	965	1599	33	94892982	2537	2872	35	3130050H1	4980	5253
33	70919147V1	975	1630	33	92410925	2550	2875	35	6342848H1	4981	5253
33	70920073V1	974	1610	33	9652629	2559	2857	35	9866163	4979	5254
33	70917224V1	1001	1557	33	5316017H1	2581	2854	35	143138F1	4992	5258
33	9988490	1047	1351	33	5316857H1	2585	2854	35	93755072	4993	5261
33	71272983V1	1049	1459	33	5318171H1	2597	2854	35	9880989	4994	5263
33	71031330V1	1104	1535	33	92337727	2598	2873	35	9877984	5006	5255
33	4156408F6	1156	1557	33	756115T6	2617	2848	35	1749391T6	4740	5217
33	4156408H1	1156	1423	33	4735116H1	2631	2876	35	1344542H1	4747	5062
33	71031387V1	1159	1604	33	1365975R6	2632	2872	35	95176036	4752	5258
33	5998189H1	1177	1292	33	1365975H1	2632	2872	35	5595877H1	4753	4917
33	71273906V1	1179	1753	33	1365975T6	2633	2853	35	6505354H1	4757	5265
33	2791668F6	1216	1550	33	91211220	2687	2875	35	1880971T6	4758	5218
33	2791668H1	1216	1544	33	2560064H1	2725	2872	35	95675620	4765	5258
33	6609076H2	1	541	33	9988325	2753	2845	35	94372792	4767	5256
33	2807474H1	7	182	34	3373528H1	609	720	35	94281732	4769	5257
33	6491123H1	19	165	34	95754867	731	968	35	95810326	4772	5259
33	6783159H1	27	590	34	2045586H1	1036	1288	35	94999023	4773	5253
33	91727301	32	157	34	6799054H1	1	622	35	5097726H1	4779	5029
33	6828289H1	438	965	34	6452403H2	29	524	35	5685655H1	4778	5025
33	3674253H1	471	632	34	91978677	101	420	35	93086706	4784	5259
33	6953528H1	597	886	34	6982612H1	143	724	35	93752346	4790	5264
33	70917171V1	645	1168	34	3359232H1	147	369	35	2183473H1	4792	5046
33	2791572H1	646	934	34	6834663H1	387	1001	35	93016110	4805	5260
33	756115F1	2364	2872	34	7001130H1	504	866	35	6751216H1	4811	5148
33	95658477	2374	2795	34	7318752H1	574	1174	35	5325018H1	4813	5082
33	92324579	2375	2789	35	1999073H1	4939	5184	35	5321404T9	4813	5124
33	2748719H1	2415	2696	35	94330742	4944	5258	35	5323707H1	4813	5089
33	94533354	2425	2876	35	4934920H1	4945	5258	35	5321503H1	4813	5077
33	94564567	2440	2876	35	94393289	4948	5263	35	95921006	4814	5258
33	4829083H1	2441	2731	35	1659543H1	4959	5214	35	5477528H1	4813	5119
33	95528721	2457	2877	35	93118267	4973	5261	35	5482768H1	4813	5046
33	9788300	2535	2872	35	95849381	4977	5259	35	5475712H1	4813	5014
33	94283575	2524	2872	35	91218351	4988	5256	35	5323312H1	4813	5048

TABLE 4 (cont.)

35	95511339	4816	5258	35	9847184	4909	5228	35	9434467	4329	4560
35	96036549	4817	5262	35	2198423T6	4911	5218	35	1749391F6	4332	4392
35	6337194H1	4817	4949	35	7063034H1	4916	5253	35	1749391H1	4332	4386
35	96399777	4829	5263	35	5485489H1	4916	5210	35	701985H1	4412	4611
35	96117467	4829	5264	35	1690630H1	4920	5157	35	4407419H1	4419	4685
35	94435700	4839	5258	35	95888136	4922	5258	35	4708563H1	4446	4698
35	95636554	4842	5258	35	723564H1	4923	5070	35	6852905H1	4459	5027
35	93594269	4843	5258	35	723580H1	4923	5158	35	6264623H1	4490	5031
35	94073072	4859	5258	35	91860289	4937	5258	35	3640801H1	4504	4758
35	92458074	4844	5260	35	1568070H1	4938	5172	35	2744645H1	4504	4757
35	94533318	4845	5258	35	2775811H1	4069	4341	35	1879458H1	4505	4778
35	92987667	4847	5212	35	2836761H1	4073	4337	35	7287970H1	4530	5048
35	1924391R6	4847	5258	35	92070265	4078	4492	35	6333393H1	4550	5092
35	1924391T6	4847	5218	35	6812440H1	4090	4428	35	144995H1	4591	4772
35	1924391H1	4847	5074	35	6812440J1	4090	4428	35	3147774H1	4595	4831
35	92555756	4854	5257	35	3151404H1	4109	4352	35	6329285H1	4599	5271
35	92054443	4858	5258	35	6033478H1	4116	4485	35	661058H1	4600	4880
35	5771260H1	4874	5258	35	92878580	4117	4402	35	1834059R6	4601	5054
35	2246911H1	4872	5159	35	93050962	4115	4372	35	1834059H1	4601	4873
35	91267895	4883	5266	35	6273920H2	4141	4414	35	6158436H1	4618	4903
35	1339830H1	4883	5135	35	1701815H1	4143	4330	35	1622370H1	4620	4876
35	95590233	4886	5257	35	6426867H1	4156	4711	35	91423847	4624	4905
35	94303732	4888	5259	35	6427663H1	4178	4711	35	4576478H1	4629	4893
35	92054335	4892	5260	35	3368975H1	4198	4330	35	600650H1	4631	4922
35	6722884H1	4893	5253	35	94125826	4225	4670	35	3316972H1	4638	4904
35	91471105	4897	5262	35	1531459H1	4225	4418	35	6954952H1	4640	5237
35	92963543	4895	5261	35	2966424H1	4227	4330	35	2759067H1	4643	4939
35	94900893	4896	5263	35	2684363H1	4237	4393	35	555514H1	4650	4902
35	9775422	4901	5265	35	2116137H1	4273	4382	35	5334364H1	4650	4864
35	95362828	4902	5258	35	669344H1	4290	4560	35	5334363H1	4650	4806
35	95396797	4907	5264	35	2672272H1	4314	4418	35	91367753	4648	5254
35	3164806H1	4904	5221	35	1453860H1	4326	4539	35	3526337H1	4662	4986
35	95766150	4907	5251	35	1453827H1	4326	4491	35	4864025H1	4665	4953
35	2252371H1	4909	5155	35	6179108H1	4330	4609	35	3803045H1	4668	4966

TABLE 4 (cont.)

35	4002622H1	4679	4784	35	2040433H1	5115	5221	35	2708492H1	2897	2999
35	836008H1	4687	4806	35	4018392H1	5123	5241	35	6463093H1	2925	3110
35	2957630H1	4690	4989	35	92079096	5140	5258	35	7091379H1	2969	3492
35	2954183H1	4690	4974	35	1453775H1	5143	5258	35	91741484	3051	3230
35	6202637H1	4712	5026	35	6536539H1	5171	5253	35	3284115H1	3094	3353
35	6202437H1	4710	5128	35	504486H1	5177	5246	35	1517309H1	3246	3455
35	2264722H1	4710	4941	35	95554333	1	198	35	6952950H1	3295	3883
35	2264938H1	4710	4910	35	7030014H1	75	512	35	3216127H1	3291	3579
35	93675124	4711	5225	35	6984009H1	91	612	35	7174368H1	3332	3903
35	6862550H1	4721	5249	35	92224552	197	5260	35	3402651H1	3332	3589
35	4941757H1	4711	5007	35	7092379H1	285	473	35	7259765H1	3388	4023
35	1478716H1	4711	4940	35	7193755H2	513	1006	35	6604779H1	3511	3997
35	1476588H1	4711	4915	35	6776509H1	515	1049	35	1593761H1	3512	3747
35	1476596H1	4711	4914	35	660357H1	525	791	35	7107055H1	3521	3579
35	143138H1	4717	4918	35	661029H1	525	797	35	7199042H1	3532	4116
35	145092H1	4717	4897	35	6990425H1	538	887	35	6988147H1	3534	3899
35	9395766	4724	5078	35	5623310H1	656	986	35	6806336J1	3535	4013
35	1834059T6	4728	5218	35	6939255H1	673	1165	35	6806336H1	3536	3983
35	6393179H1	4736	5021	35	6776509J1	970	1578	35	7032229H1	3569	4118
35	6386330H1	4737	5011	35	5629345H1	1070	1249	35	3120776H1	3582	3716
35	9866953	5008	5258	35	6348743H1	1585	1860	35	3745702H1	3587	3892
35	9867451	5014	5259	35	6774260J1	1597	2124	35	3745703H1	3589	3889
35	3865585H1	5017	5263	35	6765277H1	1861	2427	35	7323378H1	3724	4337
35	92263181	5033	5257	35	6774260H1	1904	2321	35	7032660H1	3722	4284
35	91741383	5041	5258	35	6516341H1	2086	2424	35	3532688H1	3747	3964
35	93889402	5037	5258	35	7012981H1	2178	2351	35	6534296H1	3784	4031
35	95444119	5046	5266	35	7075422H1	2231	2823	35	1661311H1	3802	3897
35	2117462H1	5071	5195	35	7185631H1	2343	2765	35	2198423H1	3826	3970
35	917065H1	5073	5258	35	3101228H1	2529	2835	35	1880971F6	3829	4311
35	95637280	5073	5257	35	6036945H1	2608	3124	35	1880971H1	3829	4098
35	917065T1	5073	5239	35	6637659H1	2635	3204	35	1555666H1	3881	4099
35	92464570	5078	5258	35	7331036H1	2646	3182	35	1517127H1	3898	4106
35	92016352	5088	5258	35	6637659J1	2647	3193	35	3170592H1	3940	4237
35	5022709H1	5115	5268	35	7180283H1	2692	3235	35	6808106H1	3949	4234

TABLE 4 (cont.)

35	6808106J1	3950	4234	36	91751107	5760	6066	36	824598T6	3289	3492
35	7185914H1	3966	4388	36	9778115	5856	6056	36	92047298	3323	3838
35	6943659H1	3983	4468	36	92876940	6002	6062	36	92047291	3323	3820
35	9766595	3993	4326	36	3219151H1	5058	5386	36	7247410H1	3362	3587
36	4274433H1	3948	4086	36	3203918T6	5064	5609	36	3203918F6	3488	3984
36	7289132H1	2748	3156	36	3739027H1	5140	5358	36	3203918H1	3489	3685
36	3739607H1	2770	2954	36	2645933H1	5149	5412	36	6172362H1	3583	3870
36	2149153T6	2515	3015	36	93778574	5152	5629	36	5044786H1	3736	4008
36	91880151	2565	2784	36	94244154	5153	5624	36	70046502V1	3863	4274
36	2148724T6	2583	3030	36	94311781	5164	5626	36	70047585V1	3863	4328
36	95449141	2616	3056	36	94175659	5175	5634	36	1304976F6	3863	4282
36	1845983T6	2617	3015	36	3620939H1	5187	5481	36	1304976H1	3863	4108
36	2658150H1	2654	2950	36	5113889H1	5186	5447	36	70047549V1	3863	4010
36	93181486	2726	3061	36	2656336T6	5202	5577	36	826082R1	3920	4502
36	589633R6	2736	3083	36	5700054H1	5204	5442	36	826082H1	3920	4203
36	589633T6	2736	3029	36	5700086H1	5204	5267	36	2308804H1	2791	3054
36	93797974	2747	3063	36	91751351	5217	5521	36	9846473	2794	3065
36	6883937H1	2092	2600	36	1679842T6	5226	5584	36	91218558	2851	3063
36	6979204H1	2099	2630	36	1679842F6	5233	5624	36	7291393H1	2960	3486
36	95768436	2174	2636	36	1679842H1	5233	5434	36	6524466H1	3005	3410
36	5589055H1	2255	2525	36	92659077	5240	5584	36	6524566H1	3005	3543
36	5589206H1	2255	2510	36	95813116	5263	5626	36	1599523F6	3076	3438
36	1845983R6	2276	2760	36	92659410	5288	5628	36	1599523H1	3076	3277
36	1845983H1	2276	2541	36	94148675	5303	5627	36	91165330	3140	3528
36	9846523	2282	2754	36	92051261	5311	5630	36	7247361H1	3207	3719
36	5120292T6	2319	2628	36	1234495H1	5320	5628	36	91983706	3207	3474
36	5771030H1	2355	2872	36	2188493H1	5320	5600	36	3070168H1	2500	2795
36	819494H1	2363	2622	36	2683448T6	5334	5590	36	5519150H1	4199	4369
36	2149153F6	2494	2777	36	9840575	5338	5626	36	2717228H1	4200	4443
36	2149153H1	2494	2762	36	7245834H1	3231	3438	36	9839478	4978	5251
36	2593534T6	5664	6026	36	824598R6	3289	3534	36	6217349H1	4984	5467
36	2593534F6	5671	6070	36	891226H1	3289	3534	36	2970290H1	5053	5365
36	2593534H1	5671	5908	36	824598H1	3289	3534	36	91982712	4550	4796
36	92541279	5708	6071	36	824598T1	3289	3494	36	613186H1	4558	4795

TABLE 4 (cont.)

36	3724286H1	4560	4854	36	2683448H1	4167	4417	36	6883937J1	1	549
36	4365389H1	4562	4823	36	1300835T7	4174	4404	37	70554791V1	269	836
36	4754909H1	4583	4854	36	1307359H1	4194	4444	37	70555906V1	482	1070
36	4354479H1	4604	4869	36	2760124H1	1934	2221	37	70557145V1	488	1152
36	3330536H1	4650	4926	36	9858075	1936	2226	37	70328701D1	115	602
36	5581641H1	4650	4911	36	2760124T6	1983	2605	37	70557446V1	1746	2364
36	3528092H1	4659	4951	36	2923468H1	5441	5721	37	70557024V1	1777	2435
36	2750671H1	4685	4954	36	6838005H1	5463	5612	37	70326732D1	1800	2134
36	2668782H1	4691	4881	36	2923469T6	5476	6028	37	70326508D1	1800	1870
36	6372588H1	4723	4978	36	6838105H1	5493	5624	37	71304277V1	1830	2463
36	9778190	4793	5063	36	94333756	5545	5629	37	71156493V1	1852	2469
36	1917315H1	4825	5119	36	4502184H1	5550	5622	37	71303442V1	1864	2504
36	3621450H1	4843	5024	36	5305353H1	5567	5817	37	5542815H1	1873	2025
36	4783325H1	4844	5101	36	93647442	5625	6070	37	71157532V1	1881	2356
36	2656336F6	4877	5465	36	2733278T6	5625	6026	37	70555668V1	1893	2524
36	2656336H1	4877	5104	36	2294001H1	5633	5891	37	70555958V1	1930	2595
36	7336890H1	4913	5506	36	3993959H2	5355	5579	37	70555146V1	1931	2563
36	5920831H1	4918	5225	36	3629589H1	5367	5668	37	71303538V1	1959	2455
36	5096190H1	4963	5229	36	92051240	5401	5630	37	71304228V1	1958	2586
36	1928876H1	4970	5242	36	1599523T6	5433	5582	37	6496937H1	1967	2501
36	6217557H1	4978	5466	36	2923469F6	5441	5868	37	305090R6	1971	2342
36	5744848H1	4239	4494	36	2733278H1	745	977	37	305090H1	1970	2306
36	4176436H1	4277	4534	36	92538994	879	1084	37	4598818H1	1996	2251
36	6740355H1	4458	5003	36	7270376H1	1062	1618	37	6349213H2	2054	2378
36	3487520H1	4498	4794	36	94242829	1103	1541	37	70556404V1	1493	2023
36	3659439H1	4514	4777	36	2780338F6	1250	1717	37	3696047F6	1521	2066
36	4274741H1	3949	4251	36	2780338H1	1250	1499	37	3696047H1	1522	1818
36	4274803H1	3949	4119	36	6244653H1	1330	1838	37	71158742V1	1536	2128
36	463357H1	4010	4201	36	6308158H1	1771	2315	37	71156538V1	1542	2034
36	4314429H1	4057	4342	36	92106835	1893	2201	37	70327564D1	1550	2005
36	9920351	4116	4382	36	2760124R6	1934	2378	37	4670450H1	1563	1762
36	91149210	4133	4231	36	96330616	228	5624	37	71157870V1	1598	2195
36	3766255H1	4149	4322	36	2733278F6	745	1284	37	70556820V1	1615	2235
36	2683448F6	4167	4553	36	3994147H1	5353	5628	37	6416418H1	1667	1887

TABLE 4 (cont.)

37	6389818H1	1667	1987	37	70555710V1	602	1210	37	9209982	3028	3419
37	4518860H1	1672	1933	37	70554866V1	605	1225	37	2770719H1	3054	3325
37	70554892V1	1703	2343	37	70327790D1	614	1116	37	2770719F6	3054	3249
37	70554965V1	1703	2332	37	70325412D1	620	997	37	92077519	3061	3419
37	6830659J1	1705	2343	37	70326955D1	620	1007	37	92099950	3063	3288
37	3279857H1	1719	1993	37	6828695H1	703	1285	37	95664324	3092	3419
37	71304118V1	1741	2354	37	2868052H1	708	843	37	95452554	3115	3474
37	71158362V1	1743	2480	37	70555300V1	723	1261	37	71158855V1	1155	1627
37	71155779V1	2409	2987	37	1582746H1	3153	3386	37	5811393H1	1155	1458
37	4172634F6	2447	3014	37	95848554	3164	3419	37	71157014V1	1155	1753
37	4172634H1	2447	2722	37	2770719T6	3195	3431	37	95850365	1172	1534
37	4438947H1	2448	2716	37	6416515H1	3258	3419	37	95865429	1177	1479
37	71156387V1	2457	2883	37	94739984	3348	3419	37	70446257V1	1237	1854
37	71303533V1	2512	2939	37	6785591H1	12	523	37	70446298V1	1236	1858
37	7353820H1	2529	2887	37	2925464F6	16	568	37	70326574D1	1292	1722
37	4539057H1	2561	2815	37	4179240H1	17	287	37	70555309V1	1308	1895
37	2328218H1	2633	2899	37	2925464H1	16	274	37	70555528V1	1315	1998
37	71304436V1	2666	3213	37	4179553F8	21	514	37	70556256V1	1368	2053
37	71157628V1	2710	3265	37	4179553H1	21	247	37	70556149V1	1371	1998
37	5106567H1	2713	2961	37	4874914H1	4	263	37	70555054V1	1382	1948
37	4599088H1	2761	3020	37	4179741H1	4	294	37	70555206V1	1385	1982
37	1501621F6	2190	2690	37	6075277H1	2826	3033	37	4441126H1	1384	1659
37	1501621H1	2190	2378	37	1426361F6	2857	3303	37	70557288V1	1422	2021
37	70557357V1	2284	2914	37	1426357H1	2857	3060	37	70560338V1	1426	2013
37	71157279V1	2290	2770	37	71131546V1	2866	3169	37	70326191D1	1440	1766
37	6116935H1	2291	2555	37	5536040H1	2910	3142	37	70327556D1	1458	2005
37	70325710D1	2321	2741	37	1501621T6	2953	3435	37	3699373H1	25	340
37	70325612D1	2363	2756	37	71158019V1	2958	3419	37	70327386D1	26	382
37	70328746D1	2363	2721	37	4050931H1	2977	3284	37	6784564H2	35	536
37	71156954V1	2388	2865	37	70326238D1	2988	3419	37	6786847H2	39	668
37	761848H1	2387	2597	37	4179553T9	2999	3343	37	70554782V1	730	1378
37	2528759H1	2396	2656	37	71156430V1	3001	3419	37	70555359V1	732	1309
37	70555774V1	2404	3076	37	94665411	3004	3419	37	6830659H1	734	1265
37	3222459H1	2408	2765	37	4172634T6	3023	3429	37	70555879V1	743	1324

TABLE 4 (cont.)

37	70556961V1	761	1427	37	70326287D1	2151	2447	39	7361157H1	1029	1613
37	70557092V1	784	1383	37	71155657V1	2163	2702	39	579137H1	1293	1511
37	70554523V1	792	1538	37	4179741T9	2811	3358	39	96197626	1359	1828
37	70557219V1	804	1427	37	70556579V1	2797	3121	39	7156184J2	747	1335
37	70555075V1	854	1389	37	71303602V1	2803	3455	39	7277468H1	854	1192
37	70555282V1	856	1303	37	92051100	2822	3123	39	92986601	375	462
37	70554784V1	862	1429	38	60100196D1	1959	2231	39	5844017H1	418	618
37	6785373H1	889	1448	38	1859554H1	2167	2443	39	7324537H1	307	843
37	70556389V1	938	1426	38	1859570H1	2167	2444	39	91277998	1	466
37	70556118V1	963	1544	38	3361850H1	2214	2460	39	804517H1	25	265
37	70557489V1	1005	1631	38	5272051H1	2369	2567	39	4918488H1	31	303
37	70554717V1	1009	1418	38	5272051F9	2369	2887	39	7156184H2	35	641
37	6784929H1	1068	1464	38	5272051F8	2369	2912	39	1703886F6	35	435
37	6828695J1	1071	1726	38	5090972F6	2471	2993	39	1703886H1	35	245
37	70556000V1	1081	1742	38	5090972H1	2471	2747	39	3809668H1	45	350
37	6934607H1	1085	1599	38	4274991F6	2519	2898	39	95152120	74	458
37	70449057V1	1109	1224	38	4274991H1	2519	2780	39	4550249H1	1	264
37	71303301V1	1146	1592	38	2185660H1	2581	2841	39	96142263	81	462
37	5811393F6	1155	1729	38	5090972R6	2805	3071	39	92254363	214	462
37	71156205V1	1155	1718	38	95802614	1	3437	39	1703886T6	232	484
37	70554574V1	568	1182	38	60100191D1	1682	2005	39	2656212F6	290	462
37	70556236V1	564	1260	38	91373056	1770	2132	40	5314759H1	182	438
37	70554808V1	577	1186	38	6489031H1	1908	2435	40	6222064U1	497	1056
37	6788638H1	13	474	38	5272051T9	2893	3324	40	93003145	668	944
37	6787884H1	1	326	38	4274991T6	2954	3393	40	3818881F6	1	468
37	71303881V1	1465	2036	38	94196744	2957	3437	40	70536625V1	1	563
37	6788583H1	1	581	38	60100196B1	2968	3406	40	3818881H1	1	280
37	6788770H1	510	1086	38	60100198B1	3119	3474	40	3345551H1	83	362
37	70554811V1	2066	2662	38	60100190B1	3184	3401	40	5988985F9	102	643
37	4515767H1	2069	2207	38	93418913	3219	3438	40	5988985H1	102	378
37	71303748V1	2138	2612	38	60100191B1	3333	3472	40	6267489H1	104	741
37	70328165D1	2151	2705	39	196837H1	3382	3511	40	4072614H1	112	399
37	70326303D1	2151	2673	39	6775050J1	717	1394	40	7167692H1	120	649
					6775050H1	925	1555	41	91545026	2331	2704

TABLE 4 (cont.)

41	g1062645	2331	2693	41	2497235H1	1745	2055	42	5926529H1	5081	5401
41	g1064773	2331	2676	41	7190840H1	2160	2660	42	g1751265	5091	5420
41	g1482703	2331	2498	41	3285638H1	2171	2415	42	4767333H1	5123	5429
41	6549638H1	2430	3013	41	3285638F6	2171	2570	42	70812418V1	5132	5800
41	70300848D1	2452	2708	41	70300497D1	1250	1823	42	5833936H1	5148	5428
41	70300835D1	2479	2708	41	3348848H1	1522	1695	42	g3016077	5152	5415
41	415443H1	2572	2798	41	60133508V1	1520	1825	42	g4149219	5242	5421
41	419855H1	2572	2791	41	60131087B1	2209	2545	42	70814699V1	5281	5854
41	416163H1	2572	2762	41	70300222D1	2312	2702	42	70868813V1	5288	5908
41	1739793H1	3085	3321	41	g1482020	2331	2775	42	1373555H1	5301	5546
41	1739793T6	3100	3767	41	2897538H1	1	259	42	g4307618	5322	5811
41	4422806H1	3205	3454	41	g5457042	169	2567	42	70867023V1	5332	5966
41	415443F1	3205	3806	41	3901248T9	378	1003	42	70869633V1	5404	6021
41	70300638D1	3222	3594	41	3899909T8	440	979	42	g2409915	5411	5811
41	70300351D1	3251	3666	41	70516717D1	1091	1389	42	1433020H1	5460	5705
41	1595527T6	3300	3770	41	70300884D1	1130	1406	42	70867216V1	5558	6222
41	1595527H1	3307	3511	41	415991H1	2572	2642	42	1267718H1	4756	5019
41	415986F1	3324	3806	41	415443R1	2572	3083	42	g318200	4774	5165
41	4879243H1	3381	3654	41	6362320H1	2606	2807	42	1464866H1	3731	3992
41	g6139643	3394	3806	41	2783446H2	2623	2867	42	70870570V1	3750	4457
41	g1482608	3395	3806	41	4442155H1	2651	2857	42	71230331V1	3765	4290
41	2287181H1	3404	3604	41	1849376H1	2685	2967	42	71222361V1	3780	3934
41	2287181R6	3404	3572	41	3285638T6	2784	3315	42	71190090V1	3794	4487
41	g1162076	3447	3742	41	70300827D1	2787	3376	42	70837174V1	3808	4000
41	g1527588	3504	3806	41	g3447015	2817	3261	42	71216238V1	3533	4246
41	g1481970	3516	3806	41	2879330H1	2863	3165	42	71189613V1	3573	4128
41	5779072H1	3534	3787	41	g4110893	2891	3343	42	4147558H1	4630	4860
41	70300150D1	3556	3802	41	g6037968	2932	3343	42	71191702V1	4644	5197
41	g1062646	3606	3790	41	g3693629	2952	3343	42	3769383H1	4647	4965
41	g1064735	3701	3781	41	4113890H1	2979	3246	42	71131533V1	4665	5137
41	g4112497	3100	3288	41	70300837D1	1134	1556	42	70816797V1	4715	5387
41	684750H1	3105	3340	41	70300823D1	1230	1552	42	71188635V1	4724	5165
41	2402302H1	3037	3261	41	60211594U1	1243	1746	42	7051349H1	3739	4208
41	1739793R6	3085	3458	42	70866933V1	5034	5705	42	71189574V1	4075	4700

TABLE 4 (cont.)

42	9612859	4079	4410	42	9823731	3267	3515	42	71188785V1	4601	5195
42	71189238V1	4084	4700	42	7044511H1	3272	3873	42	1817860T6	4773	5373
42	9570718	4094	4400	42	5919091H1	3287	3555	42	71230388V1	3476	4062
42	71188405V1	4111	4753	42	71188683V1	3333	3897	42	6337414H1	4795	5436
42	92805702	4165	4597	42	71191815V1	3333	3961	42	71188365V1	4864	5408
42	93694501	4167	4598	42	71191533V1	3333	3856	42	71129972V1	4882	5273
42	71189379V1	4173	4848	42	71191734V1	3333	3854	42	93887571	4884	5422
42	96144708	4176	4598	42	1600316F6	3333	3729	42	7052610H1	3740	3875
42	92323168	4177	4598	42	1600316H1	3333	3435	42	71230123V1	4787	5357
42	9819401	4184	4610	42	70867333V1	3341	3911	42	1600316T6	4788	5379
42	70868193V1	4190	4727	42	9839823	3355	3689	42	92224630	1	6155
42	9766671	4190	4568	42	9824451	3355	3650	42	92142053	464	854
42	91516806	4197	4665	42	71190867V1	3363	3882	42	93842828	466	883
42	91525425	4197	4612	42	70870265V1	3396	4051	42	1311611F6	4886	5420
42	9830693	4218	4610	42	2013807H1	3391	3501	42	1311611T6	4886	5378
42	71188787V1	4238	4612	42	70866888V1	3809	4505	42	9575078	4886	5176
42	4785755H1	4253	4533	42	3673862H1	5564	5859	42	1311611H1	4886	5148
42	70866811V1	4297	4860	42	2499983T6	5584	6176	42	71188609V1	4890	5438
42	91614228	4303	4568	42	9815044	4346	4627	42	71229950V1	4890	5346
42	93229742	467	888	42	70869526V1	4360	4860	42	2293604H1	4890	5151
42	95457022	725	3257	42	2499983H1	4367	4635	42	621828H1	4890	5148
42	95456921	725	6222	42	70867729V1	4376	5138	42	2626661H1	4890	5070
42	94683485	1334	1781	42	5386383H1	4385	4647	42	1269521T6	4892	5380
42	95765573	1334	1759	42	70868265V1	4388	5095	42	6327560H1	4893	5348
42	93075910	1387	1688	42	6274578H1	4416	4860	42	92539162	4894	5429
42	7190218H2	2401	2913	42	71190615V1	4434	5068	42	94852194	4905	5421
42	71229788V1	2815	3413	42	70866931V1	4477	5082	42	92932593	4922	5424
42	5014904F6	2815	3221	42	7118990V1	4513	5134	42	93148673	4928	5422
42	5014904H1	2815	3090	42	71190387V1	4513	5133	42	7098720H1	4931	5587
42	71229920V1	2973	3658	42	9672203	4544	4860	42	95707120	4951	5413
42	71228807V1	3182	3779	42	1269521F6	4577	5030	42	3975608H1	4953	5272
42	6884462H1	3181	3686	42	1269521H1	4577	4812	42	3975908H1	4954	5274
42	70868094V1	3257	3948	42	71230051V1	4584	5171	42	70814653V1	4965	5676
42	70869027V1	3256	3892	42	9670126	4590	4860	42	94971769	4971	5424

TABLE 4 (cont.)

42	71188351V1	3626	4086	71190157V1	3909	4588	42	71190271V1	3599	4339
42	70838919V1	3631	4136	71230422V1	3911	4602	42	5515021R7	3622	4216
42	71188254V1	3638	4239	70868868V1	3926	4435	42	71229150V1	3622	4275
42	71189595V1	3651	3907	71191209V1	3938	4502	42	70867419V1	3623	4261
42	70870573V1	3655	4351	71229173V1	3944	4466	42	9671390	5960	6219
42	70868067V1	3679	4334	71191826V1	3939	4349	42	9820781	5971	6244
42	70867164V1	3682	4354	71188071V1	3982	4494	42	9668623	6031	6222
42	71230406V1	3685	4227	71222526V1	3993	4351	42	71221653V1	6103	6222
42	70869964V1	3682	4340	70868437V1	4000	4529	42	9882914	6021	6129
42	1817860F6	3725	4287	70867683V1	4003	4658	42	71188120V1	4750	4951
42	1817860H1	3725	4029	71190956V1	4017	4607	42	1267718F1	4756	5198
42	7050051H1	3739	4283	70867083V1	4019	4527	42	71190911V1	4733	5379
42	70816308V1	4604	5347	70869984V1	4019	4488	42	71188586V1	4756	5397
42	70813062V1	4615	5238	9775853	4047	4392	42	70869357V1	4982	5696
42	7103719H1	4627	5050	71189002V1	4049	4491	42	93756453	4981	5424
42	9883091	4613	5038	70870114V1	4057	4751	42	4776237H1	4985	5261
42	1963922R6	4615	5216	1963922T6	5617	6180	42	71190506V1	5033	5514
42	70825247V1	4615	5083	745052H1	5643	5869	42	6608393T1	5498	6138
42	70815988V1	4615	5030	3333795T6	5681	6181	42	5907377H1	5524	5800
42	70649447V1	4615	5280	4421884H1	5703	5956	42	70870592V1	5528	6173
42	70814603V1	4615	5185	94989315	5743	6225	42	70813957V1	5544	6036
42	70812386V1	4615	5163	93446159	5744	6227	42	3333795F6	5552	6027
42	70813116V1	4615	5137	95853840	5747	6219	42	3333795H1	5552	5840
42	70812591V1	4615	5112	2280040T6	5748	6175	42	71188885V1	4599	5206
42	1963922H1	4615	4860	94264936	5749	6222	42	91525426	5842	6222
42	70817149V1	4615	5238	95590548	5767	6219	42	9882983	5853	6245
42	71190973V1	3394	4015	2280040R6	5769	6222	42	9797506	5865	6230
42	70866857V1	3421	4053	2280040H1	5769	6044	42	9587184	5880	6222
42	70869712V1	3422	4110	94114692	5775	6229	42	70870719V1	5924	6239
42	71190024V1	3462	4134	2157793H1	5776	6020	42	9814957	5894	6223
42	71222510V1	3809	4002	94269881	5783	6222	42	9822523	5964	6230
42	71229550V1	3828	4582	9314938	5790	6222	42	9612999	4719	5074
42	7317184H2	3840	4515	5014904T6	5789	6175	43	92034169	2102	2394
42	71191575V1	3866	4388	91516807	5846	6222	43	5540505T7	2291	2870

TABLE 4 (cont.)

43	6377332H1	2417	2702	44	6559394H1	1811	2428	44	4562117H1	3350	3613
43	4947810H1	2612	2733	44	3382113H1	1881	2090	44	4563263H1	3352	3636
43	95006247	1	2762	44	70606021V1	1880	2259	44	70603379V1	1131	1723
43	5540505F6	953	1415	44	70879980V1	2089	2579	44	70603933V1	1153	1782
43	5540505H1	953	1146	44	2661806F6	2089	2531	44	70607414V1	1277	1412
43	92875734	2835	2940	44	2661806H1	2089	2361	44	70607363V1	1042	1396
43	93735348	2634	2945	44	70879113V1	2089	2545	44	2414751H1	3218	3489
43	5118201T6	2631	2910	44	96476309	2149	2506	44	389997H1	3676	3915
43	2749265F6	2448	2923	44	2627073H1	2160	2391	44	6357624H1	3682	3922
43	2749265H1	2448	2714	44	2627315H1	2160	2389	44	93961665	3684	3920
43	2749265T6	2551	2897	44	3901711H1	2247	2491	44	96477150	3686	3925
43	537065H1	2429	2663	44	70887530V1	2263	2344	44	1689958F6	3693	3923
44	1452312F1	3288	3835	44	6969302U1	2280	2623	44	1689958H1	3693	3907
44	70007188D1	3260	3637	44	70881572V1	2297	2821	44	1689958T6	3698	3880
44	9898311	3282	3460	44	5763849H1	2351	2873	44	1702166T6	3718	3866
44	1452312F6	3288	3736	44	7256511H1	2398	2905	44	3572311T6	3740	3872
44	1452312H1	3288	3560	44	70882796V1	2405	3030	44	94649451	3791	3915
44	2599007H1	3312	3589	44	70886211V1	2434	2594	44	4099042H2	3816	3927
44	6325947H1	3442	3749	44	70882791V1	2477	2906	44	4099042F8	3816	4438
44	840648H1	3415	3672	44	70882271V1	2478	2974	44	1243554H1	3816	3923
44	70012088D1	3420	3797	44	70881365V1	2478	2973	44	94325490	3834	3915
44	5852153H1	3426	3701	44	70003939D1	2481	2947	44	2968601H1	3954	4247
44	70604010V1	1419	2043	44	70012299D1	2481	2829	44	95810032	3494	3926
44	6952265H1	1480	2049	44	70004016D1	2481	3025	44	7255223H1	3518	3915
44	4458494F6	1493	1942	44	3572311F6	2487	3077	44	92237335	3527	3920
44	70608095V1	1492	1936	44	3572311H1	2487	2699	44	2878117H1	3530	3815
44	4458494H1	1494	1730	44	70005627D1	2487	2687	44	91400734	3536	3915
44	7255931H2	1571	1752	44	70010847D1	2517	2952	44	5104505H1	3540	3772
44	6909665J1	1608	2154	44	7336064H1	2527	2982	44	94081742	3542	3923
44	6969377U1	1616	2026	44	70880257V1	2544	3145	44	1452312T6	3546	3876
44	2272356R6	1622	1941	44	70011933D1	2553	3044	44	9898312	3565	3918
44	2272356H1	1622	1890	44	2272356T6	2566	3001	44	6499719H1	3564	3909
44	70608114V1	1801	1904	44	70888761V1	2568	2873	44	94081564	3565	3923
44	6553230H1	1811	2165	44	3011048H1	3342	3641	44	92335900	3599	3920

TABLE 4 (cont.)

44	96451467	3602	3915	684595H1	2941	3207	44	5274874H1	2829	3072
44	91521304	3605	3931	70886274V1	2982	3197	44	70007727D1	2843	3340
44	94534027	3606	3923	70886318V1	2982	3196	44	70010542D1	2843	3307
44	5790863H1	3609	3903	6722223H1	3013	3202	44	70010162D1	2843	3246
44	5789451H1	3609	3898	2806050H1	3019	3347	44	70005864D1	2843	3198
44	5787849H1	3609	3915	1702166F6	3044	3568	44	70002001D1	2843	3074
44	95528373	3621	3920	1702166H1	3044	3271	44	70002333D1	2844	3415
44	91516463	3624	3931	4980587H1	3057	3327	44	70011761D1	2844	3198
44	95912966	3660	3920	6909665H1	3076	3619	44	70001785D1	2849	3344
44	344685H1	3673	3922	4372755H1	3078	3384	44	70007867D1	2874	3336
44	2623608H1	3367	3604	6074761H1	3079	3396	44	70006872D1	2875	3344
44	840648R1	3415	3915	685902H1	2605	2829	44	70004362D1	2885	3284
44	4333836H1	3415	3703	70880726V1	2616	3181	44	70604116V1	1123	1734
44	70881547V1	3400	3921	2615527H1	2623	2881	44	2658995H1	3490	3738
44	70886619V1	3404	3634	70879436V1	2671	3129	44	70879732V1	3478	3911
44	2414749F6	3218	3747	70882269V1	2673	3180	44	93429071	3484	3920
44	70605048V1	1033	1331	70887568V1	2676	2818	44	6317128H1	3442	3575
44	7267489H1	1034	1578	70882659V1	2688	3179	44	70879089V1	3455	3925
44	6346421H1	3442	3736	1438876F1	2686	3071	44	2661806T6	3469	3883
44	6317150H1	3442	3746	1438880H1	2686	2970	44	700495H1	3477	3740
44	4897563H1	3129	3422	1438876H1	2686	2968	44	70608699V1	853	1342
44	5379052H1	3137	3362	2258046H1	2717	2963	44	70653541V1	904	1439
44	3406784H1	3145	3410	70003496D1	2721	3284	44	70607650V1	918	1337
44	70008878D1	3156	3637	70011398D1	2733	3192	44	6938224H1	924	1338
44	70608052V1	1080	1187	70882502V1	2739	3418	44	70608866V1	964	1616
44	93888759	1108	1488	70879669V1	2748	3253	44	3776430H1	3217	3522
44	2857322H1	2904	3183	70006402D1	2745	3309	44	709518H1	3215	3449
44	70881851V1	2904	3275	70004115D1	2745	3108	44	70888779V1	3218	3398
44	792748R1	2910	3533	70011055D1	2745	3198	44	872814H1	3082	3286
44	792748H1	2909	3154	70882244V1	2768	3039	44	5438843H1	3097	3403
44	793130H1	2910	3134	70007592D1	2769	2981	44	70003362D1	3164	3424
44	7159471H1	2922	3506	6479471H1	2787	3356	44	70004958D1	3165	3415
44	70880131V1	2923	3534	7054594H1	2797	3403	44	2527855H1	3178	3528
44	1541872H1	2940	3161	70879623V1	2807	3487	44	91521303	3198	3655

TABLE 4 (cont.)

44	g1517127	3198	3698	45	1524230H1	43	257
44	2414483H1	3218	3454	45	3384786H1	92	329
44	70010299D1	3248	3632	45	6055559H1	174	688
44	70005831D1	3338	3877	45	6055841H1	174	688
44	70003405D1	3101	3415	45	4509676H1	259	437
44	70007838D1	3099	3382	45	3081417H1	405	589
44	4880465H1	3100	3351	45	2952165H1	422	670
44	70012577D1	3107	3637	45	70874349V1	542	987
44	1320150H1	3127	3364				
44	70008556D1	3132	3440				
44	4181419H1	1	167				
44	6779195J1	66	705				
44	113399R6	430	794				
44	4507995F6	435	610				
44	4507995H1	436	607				
44	6831490H1	443	635				
44	6831490J1	443	635				
44	70604944V1	690	1146				
44	70607511V1	785	1414				
44	6454789H1	1287	1795				
44	70603538V1	1322	1922				
44	684735H1	1352	1601				
44	70607606V1	1355	1770				
44	70603837V1	1402	1982				
44	70006129D1	3099	3637				
45	3386984H1	1	235				
45	3087717H1	1	207				
45	4832592H1	11	232				
45	3750644H1	15	214				
45	3350574H1	18	296				
45	3150464H1	24	307				
45	3381160H1	29	281				
45	3092918H1	38	363				
45	3092958H1	38	329				

TABLE 5

SEQ ID NO:	Template ID	Tissue Distribution
1	LG:977683.1:2000FEB18	Nervous System - 21%, Skin - 19%, Embryonic Structures - 11%
2	LG:893050.1:2000FEB18	Digestive System - 40%, Hemic and Immune System - 40%, Nervous System - 20%
3	LG:980153.1:2000FEB18	Nervous System - 16%, Urinary Tract - 12%, Skin - 12%
4	LG:350398.1:2000FEB18	Digestive System - 50%, Hemic and Immune System - 50%
5	LG:475551.1:2000FEB18	Skin - 35%, Hemic and Immune System - 19%, Digestive System - 11%
6	LG:481407.2:2000FEB18	widely distributed
7	LI:443580.1:2000FEB01	Unclassified/Mixed - 60%, Connective Tissue - 17%, Endocrine System - 13%
8	LI:803015.1:2000FEB01	Urinary Tract - 63%, Respiratory System - 38%
9	LG:027410.3:2000MAY19	Respiratory System - 100%
10	LG:171377.1:2000MAY19	Unclassified/Mixed - 74%, Female Genitalia - 13%, Cardiovascular System - 10%
11	LG:352559.1:2000MAY19	Unclassified/Mixed - 71%, Digestive System - 29%
12	LG:247384.1:2000MAY19	Stomatognathic System - 39%, Musculoskeletal System - 28%, Cardiovascular System - 19%
13	LG:403872.1:2000MAY19	Nervous System - 40%, Embryonic Structures - 23%, Urinary Tract - 14%
14	LG:1135213.1:2000MAY19	Embryonic Structures - 24%, Cardiovascular System - 20%, Unclassified/Mixed - 13%
15	LG:474284.2:2000MAY19	Unclassified/Mixed - 14%
16	LG:342147.1:2000MAY19	Pancreas - 21%, Male Genitalia - 19%, Female Genitalia - 17%, Urinary Tract - 17%
17	LG:1097300.1:2000MAY19	Endocrine System - 25%, Skin - 18%, Unclassified/Mixed - 13%
18	LG:444850.9:2000MAY19	Digestive System - 28%, Connective Tissue - 20%, Exocrine Glands - 10%
19	LG:402231.6:2000MAY19	Endocrine System - 23%, Hemic and Immune System - 23%, Digestive System - 18%
20	LG:1076157.1:2000MAY19	Embryonic Structures - 50%, Endocrine System - 28%, Respiratory System - 17%
21	LG:1083142.1:2000MAY19	Germ Cells - 84%
22	LG:1083264.1:2000MAY19	Liver - 52%, Connective Tissue - 33%
23	LG:350793.2:2000MAY19	Sense Organs - 25%, Connective Tissue - 14%
24	LG:408751.3:2000MAY19	Nervous System - 39%, Sense Organs - 39%
25	LI:336120.1:2000MAY01	Nervous System - 24%, Respiratory System - 22%, Endocrine System - 18%
26	LI:234104.2:2000MAY01	Female Genitalia - 21%, Unclassified/Mixed - 17%, Nervous System - 12%
27	LI:450887.1:2000MAY01	Nervous System - 100%
28	LI:119992.3:2000MAY01	Embryonic Structures - 10%
29	LI:197241.2:2000MAY01	Connective Tissue - 26%, Endocrine System - 12%
30	LI:406860.20:2000MAY01	Digestive System - 100%
31	LI:142384.1:2000MAY01	Connective Tissue - 44%, Germ Cells - 34%
32	LI:895427.1:2000MAY01	Cardiovascular System - 20%, Urinary Tract - 14%, Skin - 13%
33	LI:757439.1:2000MAY01	Digestive System - 18%, Embryonic Structures - 13%, Sense Organs - 12%

- 34 LI:1144066.1:2000MAY01 Cardiovascular System - 59%, Exocrine Glands - 25%
- 35 LI:2436660.4:2000MAY01 Pancreas - 63%
- 36 LI:334386.1:2000MAY01 Exocrine Glands - 17%, Male Genitalia - 16%, Musculoskeletal System - 13%
- 37 LI:347572.1:2000MAY01 Digestive System - 30%, Digestive System - 23%, Respiratory System - 17%
- 38 LI:817314.1:2000MAY01 Unclassified/Mixed - 55%, Male Genitalia - 26%, Female Genitalia - 11%
- 39 LI:000290.1:2000MAY01 Female Genitalia - 54%
- 40 LI:023518.3:2000MAY01 Urinary Tract - 50%, Musculoskeletal System - 27%, Hemic and Immune System - 23%
- 41 LI:1084246.1:2000MAY01 Sense Organs - 72%
- 42 LI:1165828.1:2000MAY01 Musculoskeletal System - 19%, Germ Cells - 18%, Nervous System - 14%
- 43 LI:007302.1:2000MAY01 Connective Tissue - 29%, Respiratory System - 21%, Hemic and Immune System - 18%
- 44 LI:236386.4:2000MAY01 Skin - 30%, Female Genitalia - 11%
- 45 LI:252904.5:2000MAY01 Exocrine Glands - 20%, Nervous System - 16%, Endocrine System - 13%

TABLE 6

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability score	Annotation
46	3	263	27	815	g10764778	1e-131	phosphoinositol 3-phosphate-binding protein-2 [Homo sapiens]
					g10045840	1e-58	TPC2 [unidentified]
					g4589582	2e-28	KIAA0969 protein [Homo sapiens]
47	1	217	10	660	g6634025	1e-81	KIAA0379 protein [Homo sapiens]
					g6453538	6e-77	hypothetical protein [Homo sapiens]
					g4803678	7e-29	ankyrin (brank-2) [Homo sapiens]
48	1	716	613	2760	g7243215	0.0	KIAA1417 protein [Homo sapiens]
					g7263990	0.0	dJ93K22.1 (novel protein (contains DKFZP564B116)) [Homo sapiens]
					g7302944	5e-57	CG8060 gene product [Drosophila melanogaster]
49	3	107	60	380			
50	3	645	3	1937	g4826478	0.0	dJ37E16.2 (SH3-domain binding protein 1) [Homo sapiens]
					g861029	0.0	SH3 domain binding protein [Mus musculus]
					g7018521	0.0	hypothetical protein [Homo sapiens]
51	3	177	93	623	g6119546	1e-45	hypothetical protein; 114721-113936 [Arabidopsis thaliana]
					g6522593	3e-10	putative RNA binding protein [Arabidopsis thaliana]
					g950424	4e-10	splicing factor, arginine/serine-rich 7 [Homo sapiens]
52	1	217	79	729	g4589566	3e-34	KIAA0961 protein [Homo sapiens]
					g3970712	3e-26	zinc finger protein 10 [Homo sapiens]
					g7630121	8e-25	zinc finger protein 92 [Mus musculus]
53	3	151	3	455	g5262560	2e-35	hypothetical protein [Homo sapiens]
					g10434856	1e-29	unnamed protein product [Homo sapiens]
					g930123	9e-27	zinc finger protein (583 AA) [Homo sapiens]
54	3	193	3	581	g10438267	1e-74	unnamed protein product [Homo sapiens]
					g7290756	8e-16	CG4532 gene product [Drosophila melanogaster]
					g5705877	8e-10	POD-1 [Caenorhabditis elegans]
55	3	282	3	848	g3077703	1e-111	mitsugumin29 [Oryctolagus cuniculus]
					g3461888	1e-108	mitsugumin29 [Mus musculus]
					g3761107	1e-108	mitsugumin29 [Mus musculus]

TABLE 6 (cont.)

SEQ ID NO.	Frame	Length	Start	Stop	GI Number	Probability score	Annotation
56	2	211	2	634	g7243243	2e-44	KIAA1431 protein [Homo sapiens]
					g4567179	2e-43	BC37295_1 [Homo sapiens]
					g3445181	1e-41	R31665_2 [Homo sapiens]
57	2	366	83	1180	g9945010	1e-120	RING-finger protein MURF [Mus musculus]
					g9929937	5e-92	hypothetical protein [Macaca fascicularis]
					g10439844	1e-36	unnamed protein product [Homo sapiens]
					g7020303	0.0	unnamed protein product [Homo sapiens]
58	3	326	354	1331	g10434892	3e-79	unnamed protein product [Homo sapiens]
					g6683707	2e-31	unnamed protein product [Homo sapiens]
					g6692607	2e-69	KIAA0455 protein [Homo sapiens]
59	1	156	70	537	g5931585	9e-47	MGA protein [Mus musculus]
							T-box family member; T-box domain [Cynops pyrrhogaster]
60	2	262	239	1024	g4049463	3e-16	transcription factor TBX6 [Homo sapiens]
					g1488047	7e-12	RING finger protein [Xenopus laevis]
					g3916727	1e-11	estrogen-responsive B box protein [Homo sapiens]
61	3	132	138	533	g401763	1e-11	ataxia-telangiectasia group D-associated protein [Homo sapiens]
					g2078531	2e-71	Mlark [Mus musculus]
					g2078529	2e-70	Hlark [Homo sapiens]
					g1149523	8e-57	Neosin [Mus musculus]
					g183002	0.0	guanylate binding protein isoform I [Homo sapiens]
62	2	167	2	502	g829177	0.0	guanylate binding protein isoform II [Homo sapiens]
63	1	570	160	1869	g7023332	0.0	unnamed protein product [Homo sapiens]
					g7020737	2e-89	unnamed protein product [Homo sapiens]
					g8920240	2e-89	AK000559 hypothetical protein, similar to (U06944) PRAJA1 [Mus musculus] [Homo sapiens]
64	3	168	3	506	g2979531	2e-51	R33683_3 [Homo sapiens]

TABLE 6 (cont.)

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability score	Annotation
65	3	246	57	794	g5262560	3e-65	hypothetical protein [Homo sapiens]
					g10434856	4e-64	unnamed protein product [Homo sapiens]
					g930123	7e-56	zinc finger protein (583 AA) [Homo sapiens]
66	3	120	51	410	g4589566	2e-23	KIAA0961 protein [Homo sapiens]
					g456269	7e-22	zinc finger protein 30 [Mus musculus domesticus]
					g5080758	2e-20	BC331191_1 [Homo sapiens]
67	2	122	329	694	g10047297	7e-26	KIAA1611 protein [Homo sapiens]
					g8163824	2e-19	krueppel-like zinc finger protein HZF2 [Homo sapiens]
					g3329372	6e-19	DNA-binding protein [Homo sapiens]
68	3	428	132	1415	g6094684	0.0	similar to Kelch proteins; similar to BAA77027 (PID:g4650844) [Homo sapiens]
					g7242973	0.0	KIAA1309 protein [Homo sapiens]
69	2	307	2	922	g7243089	0.0	KIAA1354 protein [Homo sapiens]
					g8671168	1e-135	hypothetical protein [Homo sapiens]
					g8886025	1e-135	collapsin response mediator protein-5 [Homo sapiens]
70	1	198	856	1449	g8671360	1e-131	Ulip-like protein [Rattus norvegicus]
					g1864085	1e-103	glypican-5 [Homo sapiens]
					g3015542	1e-103	glypican-5 [Homo sapiens]
71	1	227	511	1191	g205800	7e-38	intestinal protein OCI-5 [Rattus norvegicus]
					g1155088	1e-06	zyxin [Homo sapiens]
					g1545954	1e-06	zyxin [Homo sapiens]
72	3	122	3	368	g576623	2e-06	ESP-2 [Homo sapiens]
					g7629994	4e-41	60S RIBOSOMAL PROTEIN L36 homolog [Arabidopsis thaliana]
					g3236242	5e-40	60S ribosomal protein L36 [Arabidopsis thaliana]
					g11908070	5e-40	60S ribosomal protein-like protein [Arabidopsis thaliana]

TABLE 6 (cont.)

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability score	Annotation
73	2	209	500	1126	g10435614 g7243089 g7242973	1e-113 1e-113 1e-107	unnamed protein product [Homo sapiens] KIAA1354 protein [Homo sapiens] KIAA1309 protein [Homo sapiens]
74	1	312	961	1896	g7243215 g7263990	1e-157 1e-157	KIAA1417 protein [Homo sapiens] dJ93K22.1 (novel protein contains DKFZP564B116) [Homo sapiens]
75	3	190	3	572	g7302944 g10435919 g3327128	3e-17 6e-69 3e-33	CG8060 gene product [Drosophila melanogaster] unnamed protein product [Homo sapiens] KIAA0657 protein [Homo sapiens]
76	3	295	3	887	g10436504 g10436290 g10436002 g8489831	4e-09 1e-105 6e-99 2e-27	unnamed protein product [Homo sapiens] unnamed protein product [Homo sapiens] unnamed protein product [Homo sapiens] ubiquitin-conjugating BIR-domain enzyme APOLLON [Homo sapiens]
77	2	288	374	1237	g3184264 g10435546 g6653742	5e-94 5e-84 4e-54	F02569_2 [Homo sapiens] unnamed protein product [Homo sapiens] 7h3 protein [Homo sapiens]
78	1	294	97	978	g7670362 g6175860 g6330555	1e-106 4e-15 1e-13	unnamed protein product [Mus musculus] g1-related zinc finger protein [Mus musculus] KIAA1214 protein [Homo sapiens]
79	3	196	3	590	g3513300 g3882281 g10567164	3e-65 3e-50 4e-50	F16601_1, partial CDS [Homo sapiens] KIAA0780 protein [Homo sapiens] gene amplified in squamous cell carcinoma-1 [Homo sapiens]
80	3	745	285	2519	g2224553 g4210501 g10728201	0.0 0.0 3e-20	KIAA0306 [Homo sapiens] BC85722_1 [Homo sapiens] CG2779 gene product [Drosophila melanogaster]
81	3	256	507	1274	g6330617 g7301689	1e-132 2e-72	KIAA1223 protein [Homo sapiens] CG10011 gene product [Drosophila melanogaster]
					g4803678	2e-33	ankyrin (brank-2) [Homo sapiens]

TABLE 6 (cont.)

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability score	Annotation
82	1	235	841	1545	g9802433	2e-76	ACE-related carboxypeptidase ACE2 [Homo sapiens]
					g5817160	2e-76	hypothetical protein [Homo sapiens]
					g11876766	2e-76	unnamed protein product [Homo sapiens]
83	1	617	229	2079	g6665594	0.0	trp-related protein 4 truncated variant delta [Homo sapiens]
					g6665592	0.0	trp-related protein 4 truncated variant beta [Homo sapiens]
					g6665590	0.0	trp-related protein 4 [Homo sapiens]
84	3	293	735	1613	g7242977	1e-143	KIAA1311 protein [Homo sapiens]
					g912755	2e-15	B0336.3 gene product [Caenorhabditis elegans]
					g7298595	8e-12	CG10084 gene product [Drosophila melanogaster]
85	3	276	30	857	g3955100	2e-74	vacuolar adenosine triphosphatase subunit D [Mus musculus]
					g1226235	2e-74	Ac39/physophilin [Mus musculus]
					g736727	2e-74	32 kd accessory protein [Bos taurus]
86	3	355	1392	2456	g5457043	0.0	protocadherin beta 4 [Homo sapiens]
					g11142065	0.0	protocadherin beta 9 [Homo sapiens]
					g8926617	0.0	protocadherin 3H [Homo sapiens]
87	2	745	716	2950	g5457023	0.0	protocadherin alpha 9 short form protein [Homo sapiens]
					g3540157	0.0	KIAA0345-like 5 [Homo sapiens]
					g2224631	0.0	KIAA0345 [Homo sapiens]
88	2	781	50	2392	g5006248	0.0	TLR6 [Homo sapiens]
					g11596326	0.0	toll-like receptor 6 [Mus musculus]
					g5006250	0.0	TLR6 [Mus musculus]
89	2	293	1313	2191	g6164628	2e-27	SH3 and PX domain-containing protein SH3PX1 [Homo sapiens]
					g5327052	2e-27	dJ403L10.1 (SNX9 (Sorting Nexin 9)) [Homo sapiens]
					g4689258	2e-27	sorting nexin 9 [Homo sapiens]

TABLE 6 (cont.)

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability score	Annotation
90	1	241	214	936	g7022971	1e-62	unnamed protein product [Homo sapiens]
					g3882311	4e-15	KIAA0795 protein [Homo sapiens]
					g4539520	4e-14	dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) <i>J. Mol. Biol.</i> 215:403-410; Altschul, S.F. et al. (1997) <i>Nucleic Acids Res.</i> 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, ifastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) <i>Proc. Natl. Acad. Sci. USA</i> 85:2444-2448; Pearson, W.R. (1990) <i>Methods Enzymol.</i> 183:63-98; and Smith, T.F. and M.S. Waterman (1981) <i>Adv. Appl. Math.</i> 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fasta E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLOCKS IMPROVED Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) <i>Nucleic Acids Res.</i> 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) <i>Methods Enzymol.</i> 266:88-105; and Attwood, T.K. et al. (1997) <i>J. Chem. Inf. Comput. Sci.</i> 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) <i>J. Mol. Biol.</i> , 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) <i>Nucleic Acids Res.</i> 26:320-322; Durbin, R. et al. (1998) <i>Our World View</i> , in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less Signal peptide hits: Score= 0 or greater

Table 7 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score > GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. on Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence Press, Menlo Park, CA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group
5 consisting of:
 - a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45,
 - b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45,
 - c) a polynucleotide sequence complementary to a),
 - 10 d) a polynucleotide sequence complementary to b), and
 - e) an RNA equivalent of a) through d).
2. An isolated polynucleotide of claim 1, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-45.
15
3. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 1.
4. A composition for the detection of expression of disease detection and treatment molecule
20 polynucleotides comprising at least one of the polynucleotides of claim 1 and a detectable label.
5. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 1, the method comprising:
 - a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction
25 amplification, and
 - b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.
6. A method for detecting a target polynucleotide in a sample, said target polynucleotide
30 comprising a sequence of a polynucleotide of claim 1, the method comprising:
 - a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

7. A method of claim 5, wherein the probe comprises at least 30 contiguous nucleotides.

5

8. A method of claim 5, wherein the probe comprises at least 60 contiguous nucleotides.

9. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 1.

10

10. A cell transformed with a recombinant polynucleotide of claim 9.

11. A transgenic organism comprising a recombinant polynucleotide of claim 9.

15

12. A method for producing a disease detection and treatment molecule polypeptide, the method comprising:

a) culturing a cell under conditions suitable for expression of the disease detection and treatment molecule polypeptide, wherein said cell is transformed with a recombinant polynucleotide of claim 9, and

20

b) recovering the disease detection and treatment molecule polypeptide so expressed.

13. A purified disease detection and treatment molecule polypeptide (MDDT) encoded by at least one of the polynucleotides of claim 2.

25

14. An isolated antibody which specifically binds to a disease detection and treatment molecule polypeptide of claim 13.

15. A method of identifying a test compound which specifically binds to the disease detection and treatment molecule polypeptide of claim 13, the method comprising the steps of:

30

a) providing a test compound;

b) combining the disease detection and treatment molecule polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and

c) detecting binding of the disease detection and treatment molecule polypeptide to the test compound, thereby identifying the test compound which specifically binds the disease detection and treatment molecule polypeptide.

5 16. A microarray wherein at least one element of the microarray is a polynucleotide of claim 3.

17. A method for generating a transcript image of a sample which contains polynucleotides, the method comprising the steps of:

10 a) labeling the polynucleotides of the sample,

b) contacting the elements of the microarray of claim 16 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and

c) quantifying the expression of the polynucleotides in the sample.

15 18. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 1, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

20 b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

19. A method for assessing toxicity of a test compound, said method comprising:

25 a) treating a biological sample containing nucleic acids with the test compound;

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 1 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 1 or fragment thereof;

30

c) quantifying the amount of hybridization complex; and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

20. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, said target polynucleotide having a sequence of claim 1.

5

21. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

22. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is
10 completely complementary to at least 60 contiguous nucleotides of said target polynucleotide

23. An array of claim 20, which is a microarray.

24. An array of claim 20, further comprising said target polynucleotide hybridized to said first
15 oligonucleotide or polynucleotide.

25. An array of claim 20, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

20 26. An array of claim 20, wherein each distinct physical location on the substrate contains multiple nucleotide molecules having the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another physical location on the substrate.

25 27. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- a) an amino acid sequence selected from the group consisting of SEQ ID NO:46-90,
- b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:46-90,
- 30 c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:46-90, and
- d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:46-90.

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 PANZER, Scott R.
 SPIRO, Peter A.
 BANVILLE, Steven C.
 SHAH, Purvi
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 CHANG, Simon C.
 CHEN, Alice
 D'SA, Steven A.
 AMSHEY, Stefan
 DAHL, Christopher R.
 DAM, Tam C.
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 JONES, Anissa L.
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 RUSSO, Frank D.
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 DAFFO, Abel
 WRIGHT, Rachel J.
 YAP, Pierre E.
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 <212> DNA
 <213> Homo sapiens

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 <223> Incyte ID No: LG:350398.1:2000FEB18

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 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: LG:475551.1:2000FEB18

<220>

<221> unsure

<222> 424-425

<223> a, t, c, g, or other

<400> 5

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<210> 6

<211> 1801

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<400> 6

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```

```

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ttttattttt ggataaagac tctgcacaaa actgtaccag ggcaataaac aacaaacagt 420
tatttggtag agtgataaaa gcaagcattg ctattgacaa tgggaagagca gctgagttca 480
tccgaaggcg aaactacttt gataaatcta agtgttatga atgtggggaa agtggacact 540
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g 1801

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<210> 7
<211> 730
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<223> Incyte ID No: LI:443580.1:2000FEB01

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<220>
<221> unsure
<222> 44
<223> a, t, c, g, or other

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<400> 7
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gtaataatta cccgtgaaga catgtctact tttattcagc ccacatttct tattccacct 600
caaaaaacta tgagtgaaga gaaaccatgg gaatgtaaga tatgtggaaa gacctthaat 660
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aaggaaaaaa 730

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```

<210> 8
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LI:803015.1:2000FEB01

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```

<400> 8

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```

```

<210> 9
<211> 582
<212> DNA
<213> Homo sapiens

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```

<220>
<221> misc_feature
<223> Incyte ID No: LG:027410.3:2000MAY19

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```

```

<210> 10
<211> 848
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> Incyte ID No: LG:171377.1:2000MAY19

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<400> 10
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```

```

<210> 11
<211> 636
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> Incyte ID No: LG:352559.1:2000MAY19

```

```

<400> 11
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```

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```

```

<210> 12
<211> 2110
<212> DNA
<213> Homo sapiens

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```

<220>
<221> misc_feature
<223> Incyte ID No: LG:247384.1:2000MAY19

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<210> 13
<211> 2375
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: LG:403872.1:2000MAY19

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<220>
<221> unsure
<222> 1233
<223> a, t, c, g, or other

<400> 13
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<210> 14
<211> 537
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1135213.1:2000MAY19

<400> 14
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gaggagaaac agcagattat attggctaata caagatggtg gaacagtggc aggagcagca 180
cctaccttct ttgtcatctt aaagcagcca ggaaatggca aaactgatca aggaattttg 240
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<210> 15
 <211> 1433
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:474284.2:2000MAY19

<400> 15
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 gctgtacaaa ctcgagttag acaagcgcct ggtggaggag aaagtgaacc aactgaagga 720
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<210> 16
 <211> 654
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:342147.1:2000MAY19

<400> 16
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 ggagtattga ggtcactttt atattgtcct ggatagtatg tagttacgcg gtttgtaaag 240
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 ggcgctgccc gtgcgccagg tgcggacgga ccccgcccc ttttcgggtg tgcctagacgt 540
 gaagcacttc tcgcccggag acattgctgt caaggtgggtg ggcgaacacg tggagggtgca 600
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<210> 17
 <211> 1651
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1097300.1:2000MAY19

<400> 17

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catcaacgcg	gaagccagca	agaacaagag	caaagcccca	accaagttac	acgtgggcaa	300
catcagcccc	acctgcacca	accaagagct	tcgagccaag	tttgaggagc	acggtcgggc	360
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gctgggtggt	ctcttccatt	ctgttttagc	tggaaataat	agattatggt	taccgctctt	600
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<210> 18
 <211> 1870
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:444850.9:2000MAY19

<220>
 <221> unsure
 <222> 1865, 1867
 <223> a, t, c, g, or other

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gagaagtgac	agaaacaact	ttacctggac	tgaagataaa	agcacagaca	agagaacaat	180
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aaaananaaa						1870

<210> 19
 <211> 628
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:402231.6:2000MAY19

<220>
 <221> unsure
 <222> 580, 592
 <223> a, t, c, g, or other

<400> 19	gcgctctctt	ttccaggatc	atccagcagc	tcgtcaacgg	catcatcagc	cccgccacca	60
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	ccaacggcct	ggatgccatc	atcacacagc	tcctcaatca	gtttgaaaac	acaggccccc	180
	caccggcaga	taaagagaaa	atccaggccc	tcccaccgt	ccccgtcact	gaggagcacg	240
	taggctccgg	gctcagtgct	cctgtgtgca	aggacgacta	cgcgctgggt	gagcgtgtgc	300
	ggcagttgcc	ctgcaaccac	ctgttccaca	caacatacga	gcaggcctgg	ctggagcagc	360
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	ctggcctcac	tgggggtgagc	ttctcctcct	cgtcgtcctc	gtcctcctcc	agctcgccca	480
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	ctttcccacc	caccctcagc	cagcgcacac	cggcaccan	agactgggtg	cnccggcgcc	600
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<210> 20
 <211> 798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1076157.1:2000MAY19

<220>
 <221> unsure
 <222> 777
 <223> a, t, c, g, or other

<400> 20	aaaaaaaaat	tgctttatgg	aagaaagtaa	gtatagacag	agagaaaggg	atctgatgac	60
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	accagtggc	ttttaaggat	gtggctgtga	acttcaccca	ggaggagtgg	gctttgctgg	240
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	aagcaaaatc	atgtgataac	tttgtatgtg	gagaagttgg	cataggtaac	tcattcttta	540
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	agccatataa	gtgtcaacaa	cctaagaaag	ccttcagata	tcaccctcc	tttagaacac	660
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<210> 21
 <211> 410
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1083142.1:2000MAY19

<220>
 <221> unsure
 <222> 51
 <223> a, t, c, g, or other

<400> 21
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 ttcaggaatt agtgacattc agggatgtgg ccatagactt ctctcggcag gagggggaat 180
 acctggaccc taatcagagg gacttataca gggatgtgat gttggagaac tatagaaacc 240
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 gaaaagagcc ctggatgatt ttgaggggaag aaacacagtt cacagatttg gatttacagt 360
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<210> 22
 <211> 819
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1083264.1:2000MAY19

<400> 22
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 cgagccagtt tccagcccac agaaaatgag ctcttccgga agtgggcatc ttattccaat 180
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 aaatthtaag aaagggagaa taaagtgaaa aaaatctcag aaggaatcca ctcaacagac 360
 gaggattcac ttccaaagag acatattatg caaggaagca acttggaga ggaaagaaaa 420
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<210> 23
 <211> 2516
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:350793.2:2000MAY19

<220>
 <221> unsure
 <222> 85, 118, 146
 <223> a, t, c, g, or other

<400> 23
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 aaaatttagg aaattcaact taagaaacca ttatttactt ggatgatggt gaatagtaca 2520
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<210> 44
 <211> 4438
 <212> DNA
 <213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LI:236386.4:2000MAY01

<220>
<221> unsure
<222> 3774
<223> a, t, c, g, or other

<400> 44
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tgtgagagcc tcccaaagcg agagccgcca aaagaatctg ggagccagag ggacatccga 240
gcocctgccg ggtttctgga atggtggttt cagagtgagt ctcttctatt ttagaacgtt 300
gttccagtgg aaagtgtcga atttttcccc tgcgagggca gatttctcca ggtcacttga 360
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atagggcagt ttctgggcca tggacattgc tttgaagagg ggggagactgg acagcatctg 540
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gcgagtgcac tcttggactg ccttgtgagc atccccggte tgggcaggac cctctccttc 660
ccatctttt ataccacca gccagccat ggcactgaaa ggccgagccc tctatgactt 720
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cgagaactca cttggattgg ttggcttga gggccaaaac agccgtgggg agacagggt 840
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aggacaatta atagatgggt gctcctctcc ccaaggagcc atgccctggc cttgcccttg 4320
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<210> 45
<211> 987
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LI:252904.5:2000MAY01

<400> 45
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tgtggccctg gcagaatcaa gatgaggccc tgtcatgcct cccagtgag gcctacagtc 180
tgagcagaca gcatggcctg cactggcag tgaacacat gtctgcagga ggtggccggg 240
cctttgcttg atggtatggt gtatgctctg gggggaatgg gcctgacac ggccccccag 300
gcccaggtac gtgtgatga gcccgtcgg gactgtggc ttctgctacc ctccatgcc 360
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cgccagggca agctcccggg gactgctttt gaagcctttg atctggaggc ccgtacatgg 480
accgggcate caagcctacc cagecgtcgg gcctttgctg gctgcgccat ggctgaaggc 540
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cactttgtca acactgtgga gatgtttgac ctggagcatg ggtcctggac caaattgccc 660
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caagccgtgg aggcactgtg tctgcgtgat ggggtctgaa ggcttgggtg agctgtccac 960
tgagcagctc attggggatc cactagt 987

<210> 46
<211> 263
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:977683.1.orf3:2000FEB18

<400> 46
Gly Ser Asp Met Ala Ala Asp Leu Asn Leu Glu Trp Ile Ser Leu
1 5 10 15
Pro Arg Ser Trp Thr Tyr Gly Ile Thr Arg Gly Gly Arg Val Phe
20 25 30
Phe Ile Asn Glu Glu Ala Lys Ser Thr Thr Trp Leu His Pro Val
35 40 45
Thr Gly Glu Ala Val Val Thr Gly His Arg Arg Gln Ser Thr Asp
50 55 60
Leu Pro Thr Gly Trp Glu Glu Ala Tyr Thr Phe Glu Gly Ala Arg
65 70 75
Tyr Tyr Ile Asn His Asn Glu Arg Lys Val Thr Cys Lys His Pro

				80					85					90
Val	Thr	Gly	Gln	Pro	Ser	Gln	Asp	Asn	Cys	Ile	Phe	Val	Val	Asn
				95					100					105
Glu	Gln	Thr	Val	Ala	Thr	Met	Thr	Ser	Glu	Glu	Lys	Lys	Glu	Arg
				110					115					120
Pro	Ile	Ser	Met	Ile	Asn	Glu	Ala	Ser	Asn	Tyr	Asn	Val	Thr	Ser
				125					130					135
Asp	Tyr	Ala	Val	His	Pro	Met	Ser	Pro	Val	Gly	Arg	Thr	Ser	Arg
				140					145					150
Ala	Ser	Lys	Lys	Val	His	Asn	Phe	Gly	Lys	Arg	Ser	Asn	Ser	Ile
				155					160					165
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Val	Arg	Arg	Gly	Trp	Leu	Tyr
				170					175					180
Lys	Gln	Asp	Ser	Thr	Gly	Met	Lys	Leu	Trp	Lys	Lys	Arg	Trp	Phe
				185					190					195
Val	Leu	Ser	Asp	Leu	Cys	Leu	Phe	Tyr	Tyr	Arg	Asp	Glu	Lys	Glu
				200					205					210
Glu	Gly	Ile	Leu	Gly	Ser	Ile	Leu	Leu	Pro	Ser	Phe	Gln	Ile	Ser
				215					220					225
Phe	Ala	Tyr	Pro	Leu	Lys	Ile	Thr	Leu	Ile	Ala	Asn	Met	Leu	Leu
				230					235					240
Arg	Gln	Pro	Ile	Gln	Thr	Cys	Gly	Pro	Ile	Ile	Ser	Ala	Leu	Ile
				245					250					255
Gln	Glu	Arg	Lys	Trp	Ser	Cys	Gly							260

<210> 47
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:893050.1.orf1:2000FEB18

<400>	47													
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His	Leu	Glu	Val	Leu	Lys	Leu	Leu	Val	Ala	Arg	Gly	Ala	Asp	Leu
				20					25					30
Gly	Cys	Lys	Ala	Arg	Lys	Gly	Tyr	Gly	Leu	Leu	His	Thr	Ala	Ala
				35					40					45
Ala	Ser	Gly	Gln	Ile	Glu	Val	Val	Lys	Tyr	Leu	Leu	Arg	Met	Gly
				50					55					60
Ala	Glu	Ile	Asp	Glu	Pro	Asn	Ala	Phe	Gly	Asn	Thr	Ala	Leu	His
				65					70					75
Ile	Ala	Cys	Tyr	Leu	Gly	Gln	Asp	Ala	Val	Ala	Ile	Glu	Leu	Val
				80					85					90
Asn	Ala	Gly	Ala	Asn	Val	Asn	Gln	Pro	Asn	Asp	Lys	Gly	Phe	Thr
				95					100					105
Pro	Leu	His	Val	Ala	Ala	Val	Ser	Thr	Asn	Gly	Ala	Leu	Cys	Leu
				110					115					120
Glu	Leu	Leu	Val	Asn	Asn	Gly	Ala	Asp	Val	Asn	Tyr	Gln	Ser	Lys
				125					130					135
Glu	Gly	Lys	Ser	Pro	Leu	His	Met	Ala	Ala	Ile	His	Gly	Arg	Phe
				140					145					150
Thr	Arg	Ser	Gln	Ile	Leu	Ile	Gln	Asn	Gly	Ser	Glu	Ile	Asp	Cys
				155					160					165
Ala	Asp	Lys	Phe	Gly	Asn	Thr	Pro	Leu	His	Val	Ala	Ala	Arg	Tyr
				170					175					180
Gly	His	Glu	Leu	Leu	Ile	Ser	Thr	Leu	Met	Thr	Asn	Gly	Ala	Asp
				185					190					195
Thr	Gly	Arg	Arg	Gly	Ile	His	Asp	Met	Phe	Pro	Leu	His	Leu	Ala
				200					205					210
Val	Leu	Phe	Gly	Phe	Ser	Asp								215

<210> 48
 <211> 716
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:980153.1.orf1:2000FEB18

<220>
 <221> unsure
 <222> 683
 <223> unknown or other

<400> 48
 Gln Arg Gly Ala Lys Thr Arg Leu Arg Pro Phe Ser Pro Arg His
 1 5 10 15
 Cys Tyr Lys Ala Ala Thr Ile Lys Asp Val Phe Gly Arg Asn Ala
 20 25 30
 Leu His Pro Cys Phe Leu Leu Val Glu Lys Lys Gly Val Leu Asp
 35 40 45
 Trp Leu Ile Gln Lys Gly Val Asp Leu Leu Val Lys Asp Lys Glu
 50 55 60
 Ser Gly Trp Thr Ala Leu His Arg Ser Ile Phe Tyr Gly His Ile
 65 70 75
 Asp Cys Val Trp Ser Leu Leu Lys His Gly Val Ser Leu Tyr Ile
 80 85 90
 Gln Asp Lys Glu Gly Leu Ser Ala Leu Asp Leu Val Met Lys Asp
 95 100 105
 Arg Pro Thr His Val Val Phe Lys Asn Thr Asp Pro Thr Asp Val
 110 115 120
 Tyr Thr Trp Gly Asp Asn Thr Asn Phe Thr Leu Gly His Gly Ser
 125 130 135
 Gln Asn Ser Lys His His Pro Glu Leu Val Asp Leu Phe Ser Arg
 140 145 150
 Ser Gly Ile Tyr Ile Lys Gln Val Val Leu Cys Lys Phe His Ser
 155 160 165
 Val Phe Leu Ser Gln Lys Gly Gln Val Tyr Thr Cys Gly His Gly
 170 175 180
 Pro Gly Gly Arg Leu Gly His Gly Asp Glu Gln Thr Cys Leu Val
 185 190 195
 Pro Arg Leu Val Glu Gly Leu Asn Gly His Asn Cys Ser Gln Val
 200 205 210
 Ala Ala Ala Lys Asp His Thr Val Val Leu Thr Glu Asp Gly Cys
 215 220 225
 Val Tyr Thr Phe Gly Leu Asn Ile Phe His Gln Leu Gly Ile Ile
 230 235 240
 Pro Pro Pro Ser Ser Cys Asn Val Pro Arg Gln Ile Gln Ala Lys
 245 250 255
 Tyr Leu Lys Gly Arg Thr Ile Ile Gly Val Ala Ala Gly Arg Phe
 260 265 270
 His Thr Val Leu Trp Thr Arg Glu Ala Val Tyr Thr Met Gly Leu
 275 280 285
 Asn Gly Gly Gln Leu Gly Cys Leu Leu Asp Pro Asn Gly Glu Lys
 290 295 300
 Cys Val Thr Ala Pro Arg Gln Val Ser Ala Leu His His Lys Asp
 305 310 315
 Ile Ala Leu Ser Leu Val Ala Ala Ser Asp Gly Ala Thr Val Cys
 320 325 330
 Val Thr Thr Arg Gly Asp Ile Tyr Leu Leu Ala Asp Tyr Gln Cys
 335 340 345
 Lys Lys Met Ala Ser Lys Gln Leu Asn Leu Lys Lys Val Leu Val
 350 355 360
 Ser Gly Gly His Met Glu Tyr Lys Val Asp Pro Glu His Leu Lys
 365 370 375
 Glu Asn Gly Gly Gln Lys Ile Cys Ile Leu Ala Met Asp Gly Ala
 380 385 390

Gly Arg Val Phe Cys Trp Arg Ser Val Asn Ser Ser Leu Lys Gln
 395 400 405
 Cys Arg Trp Ala Tyr Pro Arg Gln Val Phe Ile Ser Asp Ile Ala
 410 415 420
 Leu Asn Arg Asn Glu Ile Leu Phe Val Thr Gln Asp Gly Glu Gly
 425 430 435
 Phe Arg Gly Arg Trp Phe Glu Glu Lys Arg Lys Ser Ser Glu Lys
 440 445 450
 Lys Glu Ile Leu Ser Asn Leu His Asn Ser Ser Ser Asp Val Ser
 455 460 465
 Tyr Val Ser Asp Ile Asn Ser Val Tyr Glu Arg Ile Arg Leu Glu
 470 475 480
 Lys Leu Thr Phe Ala His Arg Ala Val Ser Val Ser Thr Asp Pro
 485 490 495
 Ser Gly Cys Asn Phe Ala Ile Leu Gln Ser Asp Pro Lys Thr Ser
 500 505 510
 Leu Tyr Glu Ile Pro Ala Val Ser Ser Ser Ser Phe Phe Glu Glu
 515 520 525
 Phe Gly Lys Leu Leu Arg Glu Ala Asp Glu Met Asp Ser Ile His
 530 535 540
 Asp Val Thr Phe Gln Val Gly Asn Arg Leu Phe Pro Ala His Lys
 545 550 555
 Tyr Ile Leu Ala Val His Ser Asp Phe Phe Gln Lys Leu Phe Leu
 560 565 570
 Ser Asp Gly Asn Thr Ser Glu Phe Thr Asp Ile Tyr Gln Lys Asp
 575 580 585
 Glu Asp Ser Ala Gly Cys His Leu Phe Val Val Glu Lys Val His
 590 595 600
 Pro Asp Met Phe Glu Tyr Leu Leu Gln Phe Ile Tyr Thr Asp Thr
 605 610 615
 Cys Asp Phe Leu Thr His Gly Phe Lys Pro Arg Ile His Leu Asn
 620 625 630
 Lys Asn Pro Glu Glu Tyr Gln Gly Thr Leu Asn Ser His Leu Asn
 635 640 645
 Lys Val Asn Phe His Glu Asp Asp Asn Gln Lys Ser Ala Phe Glu
 650 655 660
 Val Tyr Lys Ser Asn Gln Ala Gln Thr Val Ser Glu Arg Gln Lys
 665 670 675
 Ser Lys Pro Lys Ser Cys Lys Xaa Gly Lys Asn Ile Arg Glu Asp
 680 685 690
 Asp Pro Val Arg Met Leu Gln Thr Val Ala Lys Lys Phe Asp Phe
 695 700 705
 Ser Asn Leu Ser Ser Arg Leu Asp Gly Val Arg
 710 715

<210> 49
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:350398.1.orf3:2000FEB18

<220>
 <221> unsure
 <222> 22
 <223> unknown or other

<400> 49
 Glu Pro Leu Ser Pro Pro Gly Arg Ile Pro Gly Ala Ala Gly Glu
 1 5 10
 Cys Glu Gly Pro Gln Gly Xaa Phe Ala Ser Arg Gln Pro Tyr Ser
 20 25 30
 Arg Phe Leu Leu Arg Tyr Trp His Leu Thr Pro Ile Thr Pro Trp
 35 40 45
 Ala Ile Val Pro Val Trp Ser Pro Arg Gly Arg Ser Arg Gly Ser

Pro	Asn	Ser	Thr	Ser	Gln	Thr	Ser	Ile	Gln	Ala	Gly	Thr	Ser	Thr
				50					55					60
				65					70					75
Leu	Leu	Ala	Ser	Arg	His	Gln	Asn	Ile	Trp	Glu	Asp	Met	Cys	Val
				80					85					90
Ser	Thr	Cys	Met	Trp	Gly	His	Thr	Gly	Gly	Asn	Met	Gly	Met	Arg
				95					100					105
Ala	Val													

<210> 50
 <211> 645
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:475551.1.orf3:2000FEB18

<220>
 <221> unsure
 <222> 141
 <223> unknown or other

<400> 50

Leu	Gln	Gly	Gln	Ser	Gly	Ala	Asp	Met	Asp	Lys	Arg	Val	Lys	Lys
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Leu	Pro	Leu	Met	Ala	Leu	Ser	Thr	Thr	Met	Ala	Glu	Ser	Phe	Lys
				20					25					30
Glu	Leu	Asp	Pro	Asp	Ser	Ser	Met	Gly	Lys	Ala	Leu	Glu	Met	Ser
				35					40					45
Cys	Ala	Ile	Gln	Asn	Gln	Leu	Ala	Arg	Ile	Leu	Ala	Glu	Phe	Glu
				50					55					60
Met	Thr	Leu	Glu	Arg	Asp	Val	Leu	Gln	Pro	Leu	Ser	Arg	Leu	Ser
				65					70					75
Glu	Glu	Glu	Leu	Pro	Ala	Ile	Leu	Lys	His	Lys	Lys	Ser	Leu	Gln
				80					85					90
Lys	Leu	Val	Ser	Asp	Trp	Asn	Thr	Leu	Lys	Asn	Arg	Leu	Ser	Gln
				95					100					105
Ala	Thr	Lys	Asn	Ser	Gly	Ser	Ser	Gln	Gly	Leu	Gly	Gly	Ser	Pro
				110					115					120
Gly	Ser	His	Ser	His	Thr	Thr	Met	Ala	Asn	Lys	Val	Glu	Thr	Leu
				125					130					135
Phe	Tyr	Cys	Ser	Arg	Xaa	Ser	Pro	Arg	Lys	Val	Glu	Gln	Cys	Arg
				140					145					150
Asp	Glu	Tyr	Leu	Ala	Asp	Leu	Tyr	His	Phe	Val	Thr	Lys	Glu	Asp
				155					160					165
Ser	Tyr	Ala	Asn	Tyr	Phe	Ile	Arg	Leu	Leu	Glu	Ile	Gln	Ala	Asp
				170					175					180
Tyr	His	Arg	Arg	Ser	Leu	Ser	Ser	Leu	Asp	Thr	Ala	Leu	Ala	Glu
				185					190					195
Leu	Arg	Glu	Asn	His	Gly	Gln	Ala	Asp	His	Ser	Pro	Ser	Met	Thr
				200					205					210
Ala	Thr	His	Phe	Pro	Arg	Val	Tyr	Gly	Val	Ser	Leu	Ala	Thr	His
				215					220					225
Leu	Gln	Glu	Leu	Gly	Arg	Glu	Ile	Ala	Leu	Pro	Ile	Glu	Ala	Cys
				230					235					240
Val	Met	Met	Leu	Leu	Ser	Glu	Gly	Met	Lys	Glu	Glu	Gly	Leu	Phe
				245					250					255
Arg	Leu	Ala	Ala	Gly	Ala	Ser	Val	Leu	Lys	Arg	Leu	Lys	Gln	Thr
				260					265					270
Met	Ala	Ser	Asp	Pro	His	Ser	Leu	Glu	Glu	Phe	Cys	Ser	Asp	Pro
				275					280					285
His	Ala	Val	Ala	Gly	Ala	Leu	Lys	Ser	Tyr	Leu	Arg	Glu	Leu	Pro
				290					295					300
Glu	Pro	Leu	Met	Thr	Phe	Asp	Leu	Tyr	Asp	Asp	Trp	Met	Arg	Ala
				305					310					315

Ala Ser Leu Lys Glu Pro Gly Ala Arg Leu Gln Ala Leu Gln Glu
 320 325 330
 Val Cys Ser Arg Leu Pro Pro Glu Asn Leu Ser Asn Leu Arg Tyr
 335 340 345
 Leu Met Lys Phe Leu Ala Arg Leu Ala Glu Gln Glu Val Asn
 350 355 360
 Lys Met Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu
 365 370 375
 Leu Trp Pro Pro Glu Lys Glu Gly Asp Gln Ala Gln Leu Asp Ala
 380 385 390
 Ala Ser Val Ser Ser Ile Gln Val Val Gly Val Val Glu Ala Leu
 395 400 405
 Ile Gln Ser Ala Asp Thr Leu Phe Pro Gly Asp Ile Asn Phe Asn
 410 415 420
 Val Ser Gly Leu Phe Ser Ala Val Thr Leu Gln Asp Thr Val Ser
 425 430 435
 Asp Arg Leu Ala Ser Glu Glu Leu Pro Ser Thr Ala Val Pro Thr
 440 445 450
 Pro Ala Thr Thr Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
 455 460 465
 Ala Pro Ala Leu Ala Ser Ala Ala Thr Lys Glu Arg Thr Glu Ser
 470 475 480
 Glu Val Pro Pro Arg Pro Ala Ser Pro Lys Val Thr Arg Ser Pro
 485 490 495
 Pro Glu Thr Ala Ala Pro Val Glu Asp Met Ala Arg Arg Thr Lys
 500 505 510
 Arg Pro Ala Pro Ala Arg Pro Thr Met Pro Pro Pro Gln Val Ser
 515 520 525
 Gly Ser Arg Ser Ser Pro Pro Ala Pro Pro Leu Pro Pro Gly Ser
 530 535 540
 Gly Ser Pro Gly Thr Pro Gln Ala Leu Pro Arg Arg Leu Val Gly
 545 550 555
 Ser Ser Leu Arg Ala Pro Thr Val Pro Pro Pro Leu Pro Pro Thr
 560 565 570
 Pro Pro Gln Pro Ala Arg Arg Gln Ser Arg Arg Ser Pro Ala Ser
 575 580 585
 Pro Ser Pro Ala Ser Pro Gly Pro Ala Ser Pro Ser Pro Val Ser
 590 595 600
 Leu Ser Asn Pro Ala Gln Val Asp Leu Gly Ala Ala Thr Ala Glu
 605 610 615
 Gly Gly Ala Pro Glu Ala Ile Ser Gly Val Pro Thr Pro Pro Ala
 620 625 630
 Ile Pro Pro Gln Pro Arg Pro Arg Ser Leu Ala Ser Glu Thr Asn
 635 640 645

<210> 51
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:481407.2.orf3:2000FEB18

<400> 51
 Cys Gln Gly Arg Cys Glu Arg Leu Arg Arg Val Gly Val Glu Pro
 1 5 10 15
 Gln Leu Ser Arg Gly Leu Ala Leu Phe Trp Ser Pro Arg Pro Asn
 20 25 30
 Pro Pro Glu Glu Met Ser Gly Gly Leu Ala Pro Ser Lys Ser Thr
 35 40 45
 Val Tyr Val Ser Asn Leu Pro Phe Ser Leu Thr Asn Asn Asp Leu
 50 55 60
 Tyr Arg Ile Phe Ser Lys Tyr Gly Lys Val Val Lys Val Thr Ile
 65 70 75
 Met Lys Asp Lys Asp Thr Arg Lys Ser Lys Gly Val Ala Phe Ile

				80					85					90
Leu	Phe	Leu	Asp	Lys	Asp	Ser	Ala	Gln	Asn	Cys	Thr	Arg	Ala	Ile
				95					100					105
Asn	Asn	Lys	Gln	Leu	Phe	Gly	Arg	Val	Ile	Lys	Ala	Ser	Ile	Ala
				110					115					120
Ile	Asp	Asn	Gly	Arg	Ala	Ala	Glu	Phe	Ile	Arg	Arg	Arg	Asn	Tyr
				125					130					135
Phe	Asp	Lys	Ser	Lys	Cys	Tyr	Glu	Cys	Gly	Glu	Ser	Gly	His	Leu
				140					145					150
Ser	Tyr	Ala	Cys	Pro	Lys	Asn	Met	Leu	Gly	Glu	Arg	Glu	Pro	Pro
				155					160					165
Lys	Lys	Lys	Glu	Lys	Lys	Glu	Lys	Lys	Glu	Ser	Ser			
				170					175					

<210> 52
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:443580.1.orf1:2000FEB01

<400> 52

Glu	Thr	Ser	Leu	Arg	Ser	Gly	Gln	Ile	Pro	Thr	Leu	Asp	Ser	Ser
1				5					10					15
Glu	His	Asn	Leu	Ser	Pro	Glu	Pro	Leu	Glu	Leu	Asp	Arg	Met	Pro
				20					25					30
His	Ser	Pro	Leu	Ile	Ser	Ile	Pro	His	Val	Trp	Cys	His	Pro	Glu
				35					40					45
Glu	Glu	Glu	Arg	Met	His	Asp	Glu	Leu	Leu	Gln	Ala	Val	Ser	Lys
				50					55					60
Gly	Pro	Val	Met	Phe	Arg	Asp	Val	Ser	Ile	Asp	Phe	Ser	Gln	Glu
				65					70					75
Glu	Trp	Glu	Cys	Leu	Asp	Ala	Asp	Gln	Met	Asn	Leu	Tyr	Lys	Glu
				80					85					90
Val	Met	Leu	Glu	Asn	Phe	Ser	Asn	Leu	Val	Ser	Val	Gly	Leu	Ser
				95					100					105
Asn	Ser	Lys	Pro	Ala	Val	Ile	Ser	Leu	Leu	Glu	Gln	Gly	Lys	Glu
				110					115					120
Pro	Trp	Met	Val	Asp	Arg	Glu	Leu	Thr	Arg	Gly	Leu	Cys	Ser	Asp
				125					130					135
Leu	Glu	Ser	Met	Cys	Glu	Thr	Lys	Ile	Leu	Ser	Leu	Lys	Lys	Arg
				140					145					150
His	Phe	Ser	Gln	Val	Ile	Ile	Thr	Arg	Glu	Asp	Met	Ser	Thr	Phe
				155					160					165
Ile	Gln	Pro	Thr	Phe	Leu	Ile	Pro	Pro	Gln	Lys	Thr	Met	Ser	Glu
				170					175					180
Glu	Lys	Pro	Trp	Glu	Cys	Lys	Ile	Cys	Gly	Lys	Thr	Phe	Asn	Gln
				185					190					195
Asn	Ser	Gln	Phe	Ile	Gln	His	Gln	Arg	Ile	His	Phe	Gly	Glu	Lys
				200					205					210
His	Tyr	Glu	Ser	Lys	Glu	Lys								
				215										

<210> 53
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:803015.1.orf3:2000FEB01

<400> 53

Ala	Gly	Cys	Gly	Trp	Asp	Pro	Val	Phe	Pro	Ala	Pro	Arg	Gly	Thr
1				5					10					15

Trp	Phe	Leu	Cys	Pro	Gly	Phe	Cys	His	Ser	Val	Thr	Tyr	Ala	Met
				20					25					30
Pro	Cys	Cys	Ser	His	Arg	Arg	Cys	Arg	Glu	Asp	Pro	Gly	Thr	Ser
				35					40					45
Glu	Ser	Gln	Glu	Met	Asp	Pro	Val	Ala	Phe	Asp	Asp	Val	Ala	Val
				50					55					60
Asn	Phe	Thr	Gln	Glu	Glu	Trp	Ala	Leu	Leu	Asp	Ile	Ser	Gln	Arg
				65					70					75
Lys	Leu	Tyr	Lys	Glu	Val	Met	Leu	Glu	Thr	Phe	Arg	Asn	Leu	Thr
				80					85					90
Ser	Val	Gly	Lys	Ser	Trp	Lys	Asp	Gln	Asn	Ile	Glu	Tyr	Glu	Tyr
				95					100					105
Gln	Asn	Pro	Arg	Arg	Asn	Phe	Arg	Ser	Leu	Ile	Glu	Lys	Lys	Val
				110					115					120
Asn	Glu	Ile	Lys	Asp	Asp	Ser	His	Cys	Gly	Glu	Thr	Phe	Thr	Gln
				125					130					135
Val	Pro	Asp	Asp	Arg	Leu	Asn	Phe	Gln	Glu	Lys	Lys	Ala	Ser	Pro
				140					145					150

Glu

<210> 54
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:027410.3.orf3:2000MAY19

<400>	54													
His	Thr	Glu	Ala	Arg	Pro	Pro	Arg	Arg	Glu	Ser	Trp	Ile	Ser	Asp
	1				5				10					15
Ile	Arg	Ala	Gly	Thr	Ala	Pro	Ser	Cys	Arg	Asn	His	Ile	Lys	Ser
				20					25					30
Ser	Cys	Ser	Leu	Ile	Ala	Phe	Asn	Ser	Asp	Arg	Pro	Gly	Val	Leu
				35					40					45
Gly	Ile	Val	Pro	Leu	Gln	Gly	Gln	Gly	Glu	Asp	Lys	Arg	Arg	Val
				50					55					60
Ala	His	Leu	Gly	Cys	His	Ser	Asp	Leu	Val	Thr	Asp	Leu	Asp	Phe
				65					70					75
Ser	Pro	Phe	Asp	Asp	Phe	Leu	Leu	Ala	Thr	Gly	Ser	Ala	Asp	Arg
				80					85					90
Thr	Val	Lys	Leu	Trp	Arg	Leu	Pro	Gly	Pro	Gly	Gln	Ala	Leu	Pro
				95					100					105
Ser	Ala	Pro	Gly	Val	Val	Leu	Gly	Pro	Glu	Asp	Leu	Pro	Val	Glu
				110					115					120
Val	Leu	Gln	Phe	His	Pro	Thr	Ser	Asp	Gly	Ile	Leu	Ser	Trp	Gln
				125					130					135
Pro	Met	Gly	Thr	Trp	Cys	Arg	Ala	Pro	Ser	Gly	Ala	Glu	Met	Glu
				140					145					150
Pro	Trp	Trp	Ala	Arg	Arg	Ala	Arg	Thr	Ser	Ser	Cys	Gly	Ser	Leu
				155					160					165
Thr	Pro	Glu	Gln	Ser	Arg	Gly	Pro	Leu	Arg	Ala	Arg	Arg	Pro	Met
				170					175					180
Arg	Thr	Ala	Gly	Ile	Ala	Gly	Trp	His	Gly	Trp	Ala	Pro		
				185					190					

<210> 55
 <211> 282
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:171377.1.orf3:2000MAY19

<400> 55
 Arg Pro Gln Pro Leu Arg Ala Arg Thr Ala Ala Pro Pro Arg Pro
 1 5 10 15
 Ser Gln Pro Ala Ser Gln Thr Gly Leu Arg Pro Thr Asp Gly Arg
 20 25 30
 Ser Arg Ser Gly Pro Ala Arg Leu Leu Cys Pro Gly Pro Ala Ala
 35 40 45
 Pro Arg Ser Pro Ala Val Ser Ala Ala Ser Arg Pro Glu Ser Gln
 50 55 60
 Ala Pro Thr Pro Arg Pro Ala Val Ala Ala Pro Ser Met Ser Ser
 65 70 75
 Thr Glu Arg Arg Pro Ala Gly Arg Arg Asp Arg Ser Pro Arg Gln
 80 85 90
 Gln Val Asp Arg Leu Leu Val Gly Leu Arg Trp Arg Arg Leu Glu
 95 100 105
 Glu Pro Leu Gly Phe Ile Lys Val Leu Gln Trp Leu Phe Ala Ile
 110 115 120
 Phe Ala Phe Gly Ser Cys Gly Ser Tyr Ser Gly Glu Thr Gly Ala
 125 130 135
 Met Val Arg Cys Asn Asn Glu Ala Lys Asp Val Ser Ser Ile Ile
 140 145 150
 Val Ala Phe Gly Tyr Pro Cys Arg Leu His Arg Ile Gln Tyr Glu
 155 160 165
 Met Pro Leu Cys Asp Glu Glu Ser Ser Ser Lys Thr Met His Leu
 170 175 180
 Met Gly Asp Phe Ser Ala Pro Ala Glu Phe Phe Val Thr Leu Gly
 185 190 195
 Ile Phe Ser Phe Phe Tyr Thr Met Ala Ala Leu Val Ile Tyr Leu
 200 205 210
 Arg Phe His Asn Leu Tyr Thr Glu Asn Lys Arg Phe Pro Leu Val
 215 220 225
 Asp Phe Cys Val Thr Val Ser Phe Thr Phe Phe Trp Leu Val Ala
 230 235 240
 Ala Ala Ala Trp Gly Lys Gly Leu Thr Asp Val Lys Gly Ala Thr
 245 250 255
 Arg Pro Ser Ser Leu Thr Ala Ala Met Ser Val Cys His Gly Glu
 260 265 270
 Glu Ala Val Cys Ser Ala Gly Ala Thr Pro Ser Met
 275 280

<210> 56
 <211> 211
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:352559.1.orf2:2000MAY19

<400> 56
 Val Val Ser Ser Thr Thr Ala Ser Ala Leu Gln Ser Gln Ser Lys
 1 5 10 15
 Ala Leu Leu Gln Met Lys Ser Gln Glu Glu Val Glu Val Ala Gly
 20 25 30
 Ile Lys Leu Cys Lys Ala Met Ser Leu Gly Ser Leu Thr Phe Thr
 35 40 45
 Asp Val Ala Ile Asp Phe Ser Gln Asp Glu Trp Glu Trp Leu Asn
 50 55 60
 Leu Ala Gln Arg Ser Leu Tyr Lys Lys Val Met Leu Glu Asn Tyr
 65 70 75
 Arg Asn Leu Val Ser Val Gly Leu Cys Ile Ser Lys Pro Asp Val
 80 85 90
 Ile Ser Leu Leu Glu Gln Glu Lys Asp Pro Trp Val Ile Lys Gly
 95 100 105
 Gly Met Asn Arg Gly Leu Cys Pro Asp Leu Glu Cys Val Trp Val
 110 115 120
 Thr Lys Ser Leu Ser Leu Asn Gln Asp Ile Tyr Glu Glu Lys Leu

Pro	Pro	Ala	Ile	Ile	Met	Glu	Arg	Leu	Lys	Ser	Tyr	Asp	Leu	Glu
				125					130					135
				140					145					150
Cys	Ser	Thr	Leu	Gly	Lys	Asn	Trp	Lys	Cys	Glu	Asp	Leu	Phe	Glu
				155					160					165
Arg	Glu	Leu	Val	Asn	Gln	Lys	Thr	His	Phe	Arg	Gln	Glu	Thr	Ile
				170					175					180
Thr	His	Ile	Asp	Thr	Leu	Ile	Glu	Lys	Arg	Asp	His	Ser	Asn	Lys
				185					190					195
Ser	Gly	Thr	Val	Phe	His	Leu	Asn	Thr	Leu	Ser	Tyr	Ile	Lys	Gln
				200					205					210
Ile														

<210> 57
 <211> 366
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:247384.1.orf2:2000MAY19

<400> 57

Arg	Arg	Gln	Leu	Gly	Val	Ala	Leu	Ile	Pro	Ser	His	Arg	Met	Asp
1				5					10					15
Tyr	Lys	Ser	Ser	Leu	Ile	Gln	Asp	Gly	Asn	Pro	Met	Glu	Asn	Leu
				20					25					30
Glu	Lys	Gln	Leu	Ile	Cys	Pro	Ile	Cys	Leu	Glu	Met	Phe	Thr	Lys
				35					40					45
Pro	Val	Val	Ile	Leu	Pro	Cys	Gln	His	Asn	Leu	Cys	Arg	Lys	Cys
				50					55					60
Ala	Asn	Asp	Ile	Phe	Gln	Ala	Ser	Asn	Pro	Tyr	Leu	Pro	Thr	Arg
				65					70					75
Gly	Gly	Thr	Thr	Met	Ala	Ser	Gly	Gly	Arg	Phe	Arg	Cys	Pro	Ser
				80					85					90
Cys	Arg	His	Glu	Val	Val	Leu	Asp	Arg	His	Gly	Val	Tyr	Gly	Leu
				95					100					105
Gln	Arg	Asn	Leu	Leu	Val	Glu	Asn	Ile	Ile	Asp	Ile	Tyr	Lys	Gln
				110					115					120
Glu	Cys	Ser	Ser	Arg	Pro	Leu	Gln	Lys	Gly	Ser	His	Pro	Met	Cys
				125					130					135
Lys	Glu	His	Glu	Asp	Glu	Lys	Ile	Asn	Ile	Tyr	Cys	Leu	Thr	Cys
				140					145					150
Glu	Val	Pro	Thr	Cys	Ser	Met	Cys	Lys	Val	Phe	Gly	Ile	His	Lys
				155					160					165
Ala	Cys	Glu	Val	Ala	Pro	Leu	Gln	Ser	Val	Phe	Gln	Gly	Gln	Lys
				170					175					180
Thr	Glu	Leu	Asn	Asn	Cys	Ile	Ser	Met	Leu	Val	Ala	Gly	Asn	Asp
				185					190					195
Arg	Val	Gln	Thr	Ile	Ile	Thr	Gln	Leu	Glu	Asp	Ser	Arg	Arg	Val
				200					205					210
Thr	Lys	Glu	Asn	Ser	His	Gln	Val	Lys	Glu	Glu	Leu	Ser	Gln	Lys
				215					220					225
Phe	Asp	Thr	Leu	Tyr	Ala	Ile	Leu	Asp	Glu	Lys	Lys	Ser	Glu	Leu
				230					235					240
Leu	Gln	Arg	Ile	Thr	Gln	Glu	Gln	Glu	Lys	Lys	Leu	Ser	Phe	Ile
				245					250					255
Glu	Ala	Leu	Ile	Gln	Gln	Tyr	Gln	Glu	Gln	Leu	Asp	Lys	Ser	Thr
				260					265					270
Lys	Leu	Val	Glu	Thr	Ala	Ile	Gln	Ser	Leu	Asp	Glu	Pro	Gly	Gly
				275					280					285
Ala	Thr	Phe	Leu	Leu	Thr	Ala	Lys	Gln	Leu	Ile	Lys	Ser	Ile	Val
				290					295					300
Glu	Ala	Ser	Lys	Gly	Cys	Gln	Leu	Gly	Lys	Thr	Glu	Gln	Gly	Phe
				305					310					315
Glu	Asn	Met	Asp	Phe	Phe	Thr	Leu	Asp	Leu	Glu	His	Ile	Ala	Asp

Ala	Leu	Arg	Ala	Ile	Asp	Phe	Gly	Thr	Asp	Glu	Glu	Glu	Glu	Glu	320	325	330
															335	340	345
Phe	Ile	Glu	Glu	Glu	Asp	Gln	Glu	Glu	Glu	Glu	Ser	Thr	Glu	Gly	350	355	360
Lys	Glu	Glu	Gly	His	Gln										365		

<210> 58
 <211> 326
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:403872.1.orf3:2000MAY19

<220>
 <221> unsure
 <222> 294
 <223> unknown or other

<400> 58

Glu	Met	Ala	Val	Gly	Asn	Asn	Thr	Gln	Arg	Ser	Tyr	Ser	Ile	Ile	1	5	10	15
Pro	Cys	Phe	Ile	Phe	Val	Glu	Leu	Val	Ile	Met	Ala	Gly	Thr	Val	20	25	30	35
Leu	Leu	Ala	Tyr	Tyr	Phe	Glu	Cys	Thr	Asp	Thr	Phe	Gln	Val	His	35	40	45	50
Ile	Gln	Gly	Phe	Phe	Cys	Gln	Asp	Gly	Asp	Leu	Met	Lys	Pro	Tyr	50	55	60	65
Pro	Gly	Thr	Glu	Glu	Glu	Ser	Phe	Ile	Thr	Pro	Leu	Val	Leu	Tyr	65	70	75	80
Cys	Val	Leu	Ala	Ala	Thr	Pro	Thr	Ala	Ile	Ile	Phe	Ile	Gly	Glu	80	85	90	95
Ile	Ser	Met	Tyr	Phe	Ile	Lys	Ser	Thr	Arg	Glu	Ser	Leu	Ile	Ala	95	100	105	110
Gln	Glu	Lys	Thr	Ile	Leu	Thr	Gly	Glu	Cys	Cys	Tyr	Leu	Asn	Pro	110	115	120	125
Leu	Leu	Arg	Arg	Ile	Ile	Arg	Phe	Thr	Gly	Val	Phe	Ala	Phe	Gly	125	130	135	140
Leu	Phe	Ala	Thr	Asp	Ile	Phe	Val	Asn	Ala	Gly	Gln	Val	Val	Thr	140	145	150	155
Gly	His	Leu	Thr	Pro	Tyr	Phe	Leu	Thr	Val	Cys	Lys	Pro	Asn	Tyr	155	160	165	170
Thr	Ser	Ala	Asp	Cys	Gln	Ala	His	His	Gln	Phe	Ile	Asn	Asn	Gly	170	175	180	185
Asn	Ile	Cys	Thr	Gly	Asp	Leu	Glu	Val	Ile	Glu	Lys	Ala	Arg	Arg	185	190	195	200
Ser	Phe	Pro	Ser	Lys	His	Ala	Ala	Leu	Ser	Ile	Tyr	Ser	Ala	Leu	200	205	210	215
Tyr	Ala	Thr	Met	Tyr	Ile	Thr	Ser	Thr	Ile	Lys	Thr	Lys	Ser	Ser	215	220	225	230
Arg	Leu	Ala	Lys	Pro	Val	Leu	Cys	Leu	Gly	Thr	Leu	Cys	Thr	Ala	230	235	240	245
Phe	Leu	Thr	Gly	Leu	Asn	Arg	Val	Ser	Glu	Tyr	Arg	Asn	His	Cys	245	250	255	260
Ser	Asp	Val	Ile	Ala	Gly	Phe	Ile	Leu	Gly	Thr	Ala	Val	Ala	Leu	260	265	270	275
Phe	Leu	Gly	Met	Cys	Val	Val	His	Asn	Phe	Lys	Gly	Thr	Gln	Gly	275	280	285	290
Ser	Pro	Ser	Lys	Pro	Lys	Pro	Glu	Xaa	Pro	Arg	Gly	Val	Pro	Leu	290	295	300	305
Met	Ala	Phe	Pro	Arg	Ile	Glu	Ser	Pro	Leu	Glu	Thr	Leu	Ser	Ala	305	310	315	320
Gln	Asn	His	Ser	Ala	Ser	Met	Thr	Glu	Val	Thr					320	325		

<210> 59
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1135213.1.orf1:2000MAY19

<400> 59
 Leu Cys Gly Asp Tyr Ser Cys Leu Thr Thr Glu Phe Pro Thr Glu
 1 5 10 15
 Ile Met Glu Glu Lys Gln Gln Ile Ile Leu Ala Asn Gln Asp Gly
 20 25 30
 Gly Thr Val Ala Gly Ala Ala Pro Thr Phe Phe Val Ile Leu Lys
 35 40 45
 Gln Pro Gly Asn Gly Lys Thr Asp Gln Gly Ile Leu Val Thr Asn
 50 55 60
 Gln Asp Ala Cys Ala Leu Ala Ser Ser Val Ser Ser Pro Val Lys
 65 70 75
 Ser Lys Gly Lys Ile Cys Leu Pro Ala Asp Cys Thr Val Gly Gly
 80 85 90
 Ile Thr Val Thr Leu Asp Asn Asn Ser Met Trp Asn Glu Phe Tyr
 95 100 105
 His Arg Ser Thr Glu Met Ile Leu Thr Lys Gln Gly Arg Arg Met
 110 115 120
 Phe Pro Tyr Cys Arg Tyr Trp Ile Thr Gly Leu Asp Ser Asn Leu
 125 130 135
 Lys Tyr Ile Leu Val Met Asp Ile Ser Pro Val Asp Asn His Arg
 140 145 150
 Tyr Lys Trp Asn Gly Arg
 155

<210> 60
 <211> 262
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:474284.2.orf2:2000MAY19

<400> 60
 Ser Ser Pro Thr Ser Trp Arg Ser Ser Met Pro Cys Thr Trp Arg
 1 5 10 15
 Ser Arg Arg Arg Arg Cys Thr Ala Cys Ser Ala Ala Ala Ala Pro
 20 25 30
 Pro Leu Pro Ala Gln Lys Val Cys Leu Arg Cys Glu Ala Pro Cys
 35 40 45
 Cys Gln Ser His Val Gln Thr His Leu Gln Gln Pro Ser Thr Ala
 50 55 60
 Arg Gly His Leu Leu Val Glu Ala Asp Asp Val Arg Ala Trp Ser
 65 70 75
 Cys Pro Gln His Asn Ala Tyr Arg Leu Tyr His Cys Glu Ala Glu
 80 85 90
 Gln Val Ala Val Cys Gln Tyr Cys Cys Tyr Tyr Ser Gly Ala His
 95 100 105
 Gln Gly His Ser Val Cys Asp Val Glu Ile Arg Arg Asn Glu Ile
 110 115 120
 Arg Lys Met Leu Met Lys Gln Gln Asp Arg Leu Glu Glu Arg Glu
 125 130 135
 Gln Asp Ile Glu Asp Gln Leu Tyr Lys Leu Glu Ser Asp Lys Arg
 140 145 150
 Leu Val Glu Glu Lys Val Asn Gln Leu Lys Glu Glu Val Arg Leu
 155 160 165
 Gln Tyr Glu Lys Leu His Gln Leu Leu Asp Glu Asp Leu Arg Gln
 170 175 180

Thr Val Glu Val Leu Asp Lys Ala Gln Ala Lys Phe Cys Ser Glu
 185 190 195
 Asn Ala Ala Gln Ala Leu His Leu Gly Glu Arg Met Gln Glu Ala
 200 205 210
 Lys Lys Leu Leu Gly Ser Leu Gln Leu Leu Phe Asp Lys Thr Glu
 215 220 225
 Asp Val Ser Phe Met Lys Asn Thr Lys Ser Val Lys Ile Leu Met
 230 235 240
 Asp Ser Arg Cys Pro Val His Trp Pro Gln Asp Pro Asp Leu His
 245 250 255
 Glu Gln Gln Pro Phe Pro His
 260

<210> 61
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:342147.1.orf3:2000MAY19

<400> 61
 Lys Thr Asn Leu Tyr Cys Ser Pro Tyr Phe Ile Asp Cys Asn Arg
 1 5 10 15
 Ser Ile Glu Val Thr Phe Ile Leu Ser Trp Ile Val Cys Ser Tyr
 20 25 30
 Ala Val Cys Lys Glu Arg Asn Gly Met Gly Gly Cys Glu Lys Glu
 35 40 45
 Glu Leu Val Val Asp Phe Gly Gly Ala Gly Trp Arg Ser Leu Cys
 50 55 60
 Leu Cys Ser Arg Leu Gly Cys Ala Ala Pro Arg Pro Arg Cys Pro
 65 70 75
 Asp Phe Arg Arg Pro Asp Ala Ser Leu Thr Ser Ala Ser Ala Arg
 80 85 90
 Gly Cys Trp Arg Pro Ser Trp Leu Arg Ser Ala Pro Pro Arg Ser
 95 100 105
 Pro Pro Thr Thr Cys Ala His Pro Ala Trp Arg Cys Pro Ser Pro
 110 115 120
 Arg Cys Arg Arg Thr Pro Ala Pro Phe Arg Cys Cys
 125 130

<210> 62
 <211> 167
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1097300.1.orf2:2000MAY19

<400> 62
 Pro Pro Arg Arg Arg Pro Cys Trp Phe Leu Cys Gly Leu Leu Ser
 1 5 10 15
 Arg Met Val Lys Leu Phe Ile Gly Asn Leu Pro Arg Glu Ala Thr
 20 25 30
 Glu Gln Glu Ile Arg Ser Leu Phe Glu Gln Tyr Gly Lys Val Leu
 35 40 45
 Glu Cys Asp Ile Ile Lys Asn Tyr Gly Phe Val His Ile Glu Asp
 50 55 60
 Lys Thr Ala Ala Glu Asp Ala Ile Arg Asn Leu His His His Lys
 65 70 75
 Pro His Gly Val Asn Ile Asn Ala Glu Ala Ser Lys Asn Lys Ser
 80 85 90
 Lys Ala Pro Thr Lys Leu His Val Gly Asn Ile Ser Pro Thr Cys
 95 100 105
 Thr Asn Gln Glu Leu Arg Ala Lys Phe Glu Glu His Gly Pro Ala

	110		115		120
Ile Glu Cys Asp	Ile Ala Lys Asp Tyr	Ala Phe Ala His Met	Glu		
	125		130		135
Arg Ala Glu Asp	Ala Ala Glu Ala Ile	Arg Gly Leu Asp Asn	Thr		
	140		145		150
Glu Phe Gln Gly	Glu Leu Leu Trp Ala	Trp Val Val Ala Pro	Ser		
	155		160		165
Gly Val					

<210> 63
 <211> 570
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:444850.9.orf1:2000MAY19

<220>
 <221> unsure
 <222> 569-570
 <223> unknown or other

<400> 63

Lys His Arg Gln Glu	Asn Asn Ala Leu Asp	Met Ala Pro Glu Ile	
1	5	10	15
His Met Thr Gly Pro	Met Cys Leu Ile Glu	Asn Thr Asn Gly Glu	
	20	25	30
Leu Val Ala Asn Pro	Glu Ala Leu Lys Ile	Leu Ser Ala Ile Thr	
	35	40	45
Gln Pro Val Val Val	Val Ala Ile Val Gly	Leu Tyr Arg Thr Gly	
	50	55	60
Lys Ser Tyr Leu Met	Asn Lys Leu Ala Gly	Lys Asn Lys Gly Phe	
	65	70	75
Ser Leu Gly Ser Thr	Val Lys Ser His Thr	Lys Gly Ile Trp Met	
	80	85	90
Trp Cys Val Pro His	Pro Lys Lys Pro Glu	His Thr Leu Val Leu	
	95	100	105
Leu Asp Thr Glu Gly	Leu Gly Asp Val Lys	Lys Gly Asp Asn Gln	
	110	115	120
Asn Asp Ser Trp Ile	Phe Thr Leu Ala Val	Leu Leu Ser Ser Thr	
	125	130	135
Leu Val Tyr Asn Ser	Met Gly Thr Ile Asn	Gln Gln Ala Met Asp	
	140	145	150
Gln Leu Tyr Tyr Val	Thr Glu Leu Thr His	Arg Ile Arg Ser Lys	
	155	160	165
Ser Ser Pro Asp Glu	Asn Glu Asn Glu Asp	Ser Ala Asp Phe Val	
	170	175	180
Ser Phe Phe Pro Asp	Phe Val Trp Thr Leu	Arg Asp Phe Ser Leu	
	185	190	195
Asp Leu Glu Ala Asp	Gly Gln Pro Leu Thr	Pro Asp Glu Tyr Leu	
	200	205	210
Glu Tyr Ser Leu Lys	Leu Thr Gln Gly Thr	Ser Gln Lys Asp Lys	
	215	220	225
Asn Phe Asn Leu Pro	Gln Leu Cys Ile Trp	Lys Phe Phe Pro Lys	
	230	235	240
Lys Lys Cys Phe Val	Phe Asp Leu Pro Ile	His Arg Arg Lys Leu	
	245	250	255
Ala Gln Leu Glu Lys	Leu Gln Asp Glu Glu	Leu Asp Pro Glu Phe	
	260	265	270
Val Gln Gln Val Ala	Asp Phe Cys Ser Tyr	Ile Phe Ser Asn Ser	
	275	280	285
Lys Thr Lys Thr Leu	Ser Gly Gly Ile Lys	Val Asn Gly Pro Arg	
	290	295	300
Leu Glu Ser Leu Val	Leu Thr Tyr Ile Asn	Ala Ile Ser Arg Gly	
	305	310	315

Asp Leu Pro Cys Met Glu Asn Ala Val Leu Ala Leu Ala Gln Ile
 320 325 330
 Glu Asn Ser Ala Ala Val Gln Lys Ala Ile Ala His Tyr Asp Gln
 335 340 345
 Gln Met Gly Gln Lys Val Gln Leu Pro Ala Glu Thr Leu Gln Glu
 350 355 360
 Leu Leu Asp Leu His Arg Val Ser Glu Arg Glu Ala Thr Glu Val
 365 370 375
 Tyr Met Lys Asn Ser Phe Lys Asp Val Asp His Leu Phe Gln Lys
 380 385 390
 Lys Leu Ala Ala Gln Leu Asp Lys Lys Arg Asp Asp Phe Cys Lys
 395 400 405
 Gln Asn Gln Glu Ala Ser Ser Asp Arg Cys Ser Ala Leu Leu Gln
 410 415 420
 Val Ile Phe Ser Pro Leu Glu Glu Glu Val Lys Ala Gly Ile Tyr
 425 430 435
 Ser Lys Pro Gly Gly Tyr Cys Leu Phe Ile Gln Lys Leu Gln Asp
 440 445 450
 Leu Glu Lys Lys Tyr Tyr Glu Glu Pro Arg Lys Gly Ile Gln Ala
 455 460 465
 Glu Glu Ile Leu Gln Thr Tyr Leu Lys Ser Lys Glu Ser Val Thr
 470 475 480
 Asp Ala Ile Leu Gln Thr Asp Gln Ile Leu Thr Glu Lys Glu Lys
 485 490 495
 Glu Ile Glu Val Glu Cys Val Lys Ala Glu Ser Ala Gln Ala Ser
 500 505 510
 Ala Lys Met Val Glu Glu Met Gln Ile Lys Tyr Gln Gln Met Met
 515 520 525
 Glu Glu Lys Glu Lys Ser Tyr Gln Glu His Val Lys Gln Leu Thr
 530 535 540
 Glu Lys Met Glu Arg Glu Arg Ala Gln Leu Leu Glu Glu Gln Glu
 545 550 555
 Lys Thr Leu Thr Ser Lys Leu Gln Val Ser Lys Cys Lys Xaa Xaa
 560 565 570

<210> 64
 <211> 168
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:402231.6.orf3:2000MAY19

<400> 64
 Ala Leu Phe Ser Arg Ile Ile Gln Gln Leu Val Asn Gly Ile Ile
 1 5 10 15
 Thr Pro Ala Thr Ile Pro Ser Leu Gly Pro Trp Gly Val Leu His
 20 25 30
 Ser Asn Pro Met Asp Tyr Ala Trp Gly Ala Asn Gly Leu Asp Ala
 35 40 45
 Ile Ile Thr Gln Leu Leu Asn Gln Phe Glu Asn Thr Gly Pro Pro
 50 55 60
 Pro Ala Asp Lys Glu Lys Ile Gln Ala Leu Pro Thr Val Pro Val
 65 70 75
 Thr Glu Glu His Val Gly Ser Gly Leu Glu Cys Pro Val Cys Lys
 80 85 90
 Asp Asp Tyr Ala Leu Gly Glu Arg Val Arg Gln Leu Pro Cys Asn
 95 100 105
 His Leu Phe His Thr Thr Tyr Glu Gln Ala Trp Leu Glu Gln His
 110 115 120
 Asp Ser Cys Pro Val Cys Arg Lys Ser Leu Thr Gly Gln Asn Thr
 125 130 135
 Ala Thr Asn Pro Pro Gly Leu Thr Gly Val Ser Phe Ser Ser Ser
 140 145 150
 Ser Ser Ser Ser Ser Ser Ser Ser Pro Ser Asn Glu Asn Ala Thr

Ser Asn Ser 155 160 165

<210> 65
 <211> 246
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1076157.1.orf3:2000MAY19

<220>
 <221> unsure
 <222> 240
 <223> unknown or other

<400> 65
 Pro Lys Gln Gly Ile Asn Val Trp Ser Pro Arg His Pro Glu Asn
 1 5 10 15
 Phe Leu Gly Ile Glu Ser Arg Pro Pro Met Leu Ser Leu Ser Pro
 20 25 30
 Ile Leu Leu Tyr Thr Cys Glu Met Phe Gln Asp Pro Val Ala Phe
 35 40 45
 Lys Asp Val Ala Val Asn Phe Thr Gln Glu Glu Trp Ala Leu Leu
 50 55 60
 Asp Ile Ser Gln Arg Lys Leu Tyr Arg Glu Val Met Leu Glu Thr
 65 70 75
 Phe Arg Asn Leu Thr Ser Ile Gly Lys Lys Trp Lys Asp Gln Asn
 80 85 90
 Ile Glu Tyr Glu Tyr Gln Asn Pro Arg Arg Asn Phe Arg Ser Leu
 95 100 105
 Ile Glu Gly Asn Val Asn Glu Ile Lys Glu Asp Ser His Cys Gly
 110 115 120
 Glu Thr Phe Thr Gln Val Pro Asp Asp Arg Leu Asn Phe Gln Glu
 125 130 135
 Lys Lys Ala Ser Pro Glu Ala Lys Ser Cys Asp Asn Phe Val Cys
 140 145 150
 Gly Glu Val Gly Ile Gly Asn Ser Ser Phe Asn Met Asn Ile Arg
 155 160 165
 Gly Asp Ile Gly His Lys Ala Tyr Glu Tyr Gln Asp Tyr Ala Pro
 170 175 180
 Lys Pro Tyr Lys Cys Gln Gln Pro Lys Lys Ala Phe Arg Tyr His
 185 190 195
 Pro Ser Phe Arg Thr Gln Glu Arg Asn His Thr Gly Glu Lys Pro
 200 205 210
 Tyr Ala Cys Lys Glu Cys Gly Lys Thr Phe Ile Ser His Ser Gly
 215 220 225
 Ile Arg Arg Arg Met Val Met His Ser Gly Asp Gly Pro Leu Xaa
 230 235 240
 Val Ser Phe Val Gly Lys
 245

<210> 66
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1083142.1.orf3:2000MAY19

<220>
 <221> unsure
 <222> 1
 <223> unknown or other

<400> 66
 Xaa Phe Pro Val Leu Glu Pro His Gln Val Gly Leu Ile Arg Ser
 1 5 10 15
 Tyr Asn Ser Lys Thr Met Thr Cys Phe Gln Glu Leu Val Thr Phe
 20 25 30
 Arg Asp Val Ala Ile Asp Phe Ser Arg Gln Glu Trp Glu Tyr Leu
 35 40 45
 Asp Pro Asn Gln Arg Asp Leu Tyr Arg Asp Val Met Leu Glu Asn
 50 55 60
 Tyr Arg Asn Leu Val Ser Leu Gly Gly His Ser Ile Ser Lys Pro
 65 70 75
 Val Val Val Asp Leu Leu Glu Arg Gly Lys Glu Pro Trp Met Ile
 80 85 90
 Leu Arg Glu Glu Thr Gln Phe Thr Asp Leu Asp Leu Gln Cys Glu
 95 100 105
 Ile Ile Ser Tyr Ile Glu Val Pro Thr Tyr Glu Thr Asp Ile Ser
 110 115 120

<210> 67
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:1083264.1.orf2:2000MAY19

<400> 67
 Lys Lys Ser Gln Lys Glu Ser Thr Gln Gln Thr Arg Ile His Phe
 1 5 10 15
 Gln Arg Asp Ile Leu Cys Lys Glu Ala Thr Trp Lys Arg Lys Glu
 20 25 30
 Lys Lys Ser Gly Met Ala Leu Thr Gln Gly Pro Leu Lys Phe Met
 35 40 45
 Asp Val Ala Ile Glu Phe Ser Gln Glu Glu Trp Lys Cys Leu Asp
 50 55 60
 Pro Ala Gln Arg Thr Leu Tyr Arg Asp Val Met Leu Glu Asn Tyr
 65 70 75
 Arg Asn Leu Val Ser Leu Gly Ile Cys Leu Pro Asp Leu Ser Val
 80 85 90
 Thr Ser Met Leu Glu Gln Lys Arg Asp Pro Trp Thr Leu Gln Ser
 95 100 105
 Glu Glu Lys Ile Ala Asn Asp Pro Asp Gly Arg Glu Cys Ile Gln
 110 115 120
 Lys Val

<210> 68
 <211> 428
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:350793.2.orf3:2000MAY19

<400> 68
 Ala Gln Gly Ser Ser Trp Lys Leu Pro Phe Glu Arg Leu Ala Phe
 1 5 10 15
 Val Leu Ser Ser Asn Ser Leu Lys His Cys Thr Glu Leu Glu Leu
 20 25 30
 Phe Lys Ala Thr Cys Arg Trp Leu Arg Leu Glu Glu Pro Arg Met
 35 40 45
 Asp Phe Ala Ala Lys Leu Met Lys Asn Ile Arg Phe Pro Leu Met
 50 55 60
 Thr Pro Gln Glu Leu Ile Asn Tyr Val Gln Thr Val Asp Phe Met

				65						70						75
Arg	Thr	Asp	Asn	Thr	Cys	Val	Asn	Leu	Leu	Leu	Glu	Ala	Ser	Asn		
				80						85						90
Tyr	Gln	Met	Met	Pro	Tyr	Met	Gln	Pro	Val	Met	Gln	Ser	Asp	Arg		
				95						100						105
Thr	Ala	Ile	Arg	Ser	Asp	Thr	Thr	His	Leu	Val	Thr	Leu	Gly	Gly		
				110						115						120
Val	Leu	Arg	Gln	Gln	Leu	Val	Val	Ser	Lys	Glu	Leu	Arg	Met	Tyr		
				125						130						135
Asp	Glu	Lys	Ala	His	Glu	Trp	Lys	Ser	Leu	Ala	Pro	Met	Asp	Ala		
				140						145						150
Pro	Arg	Tyr	Gln	His	Gly	Ile	Ala	Val	Ile	Gly	Asn	Phe	Leu	Tyr		
				155						160						165
Val	Val	Gly	Gly	Gln	Ser	Asn	Tyr	Asp	Thr	Lys	Gly	Lys	Thr	Ala		
				170						175						180
Val	Asp	Thr	Val	Phe	Arg	Phe	Asp	Pro	Arg	Tyr	Asn	Lys	Trp	Met		
				185						190						195
Gln	Val	Ala	Ser	Leu	Asn	Glu	Lys	Arg	Thr	Phe	Phe	His	Leu	Ser		
				200						205						210
Ala	Leu	Lys	Gly	Tyr	Leu	Tyr	Ala	Val	Gly	Gly	Arg	Asn	Ala	Ala		
				215						220						225
Gly	Glu	Leu	Pro	Thr	Val	Glu	Cys	Tyr	Asn	Pro	Arg	Thr	Asn	Glu		
				230						235						240
Trp	Thr	Tyr	Val	Ala	Lys	Met	Ser	Glu	Pro	His	Tyr	Gly	His	Ala		
				245						250						255
Gly	Thr	Val	Tyr	Gly	Gly	Val	Met	Tyr	Ile	Ser	Gly	Gly	Ile	Thr		
				260						265						270
His	Asp	Thr	Phe	Gln	Lys	Glu	Leu	Met	Cys	Phe	Asp	Pro	Asp	Thr		
				275						280						285
Asp	Lys	Trp	Ile	Gln	Lys	Ala	Pro	Met	Thr	Thr	Val	Arg	Gly	Leu		
				290						295						300
His	Cys	Met	Cys	Thr	Val	Gly	Glu	Arg	Leu	Tyr	Val	Ile	Gly	Gly		
				305						310						315
Asn	His	Phe	Arg	Gly	Thr	Ser	Asp	Tyr	Asp	Asp	Val	Leu	Ser	Cys		
				320						325						330
Glu	Tyr	Tyr	Ser	Pro	Ile	Leu	Asp	Gln	Trp	Thr	Pro	Ile	Ala	Ala		
				335						340						345
Met	Leu	Arg	Gly	Gln	Ser	Asp	Val	Gly	Val	Ala	Val	Phe	Glu	Asn		
				350						355						360
Lys	Ile	Tyr	Val	Val	Gly	Gly	Tyr	Ser	Trp	Asn	Asn	Arg	Cys	Met		
				365						370						375
Val	Glu	Ile	Val	Gln	Lys	Tyr	Asp	Pro	Asp	Lys	Asp	Glu	Trp	His		
				380						385						390
Lys	Val	Phe	Asp	Leu	Pro	Glu	Ser	Leu	Gly	Gly	Ile	Arg	Ala	Cys		
				395						400						405
Thr	Leu	Thr	Val	Phe	Pro	Pro	Glu	Glu	Thr	Thr	Pro	Ser	Pro	Ser		
				410						415						420
Arg	Glu	Ser	Pro	Leu	Ser	Ala	Pro									425

<210> 69
 <211> 307
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LG:408751.3.orf2:2000MAY19

<400>	69															
Arg	Asp	Pro	Gly	Trp	Gln	Ile	Arg	Asp	Arg	Ala	Gly	Leu	Ala	Trp		
	1			5					10					15		
Asn	Met	Leu	Ala	Asn	Ser	Ala	Ser	Val	Arg	Ile	Leu	Ile	Lys	Gly		
				20					25					30		
Gly	Lys	Val	Val	Asn	Asp	Asp	Cys	Thr	His	Glu	Ala	Asp	Val	Tyr		
				35					40					45		
Ile	Glu	Asn	Gly	Ile	Ile	Gln	Gln	Val	Gly	Arg	Glu	Leu	Met	Ile		

				50					55					60
Pro	Gly	Gly	Ala	Lys	Val	Ile	Asp	Ala	Thr	Gly	Lys	Leu	Val	Ile
				65					70					75
Pro	Gly	Gly	Ile	Asp	Thr	Ser	Thr	His	Phe	His	Gln	Thr	Phe	Met
				80					85					90
Asn	Ala	Thr	Cys	Val	Asp	Asp	Phe	Tyr	His	Gly	Thr	Lys	Ala	Ala
				95					100					105
Leu	Val	Gly	Gly	Thr	Thr	Met	Ile	Ile	Gly	His	Val	Leu	Pro	Asp
				110					115					120
Lys	Glu	Thr	Ser	Leu	Val	Asp	Ala	Tyr	Glu	Lys	Cys	Arg	Gly	Leu
				125					130					135
Ala	Asp	Pro	Lys	Val	Cys	Cys	Asp	Tyr	Ala	Leu	His	Val	Gly	Ile
				140					145					150
Thr	Trp	Trp	Ala	Pro	Lys	Val	Lys	Ala	Glu	Met	Glu	Thr	Leu	Val
				155					160					165
Arg	Glu	Lys	Gly	Val	Asn	Ser	Phe	Gln	Met	Phe	Met	Thr	Tyr	Lys
				170					175					180
Asp	Leu	Tyr	Met	Leu	Arg	Asp	Ser	Glu	Leu	Tyr	Gln	Val	Leu	His
				185					190					195
Ala	Cys	Lys	Asp	Ile	Gly	Ala	Ile	Ala	Arg	Val	His	Ala	Glu	Asn
				200					205					210
Gly	Glu	Leu	Val	Ala	Glu	Gly	Ala	Lys	Glu	Ala	Leu	Asp	Leu	Gly
				215					220					225
Ile	Thr	Gly	Pro	Glu	Gly	Ile	Glu	Ile	Ser	Arg	Pro	Glu	Glu	Leu
				230					235					240
Glu	Ala	Glu	Ala	Thr	His	Arg	Val	Ile	Thr	Arg	Asp	Gly	Gly	Asn
				245					250					255
His	Asp	Ala	Ala	Ser	Trp	Cys	Ser	Ala	His	His	Leu	Tyr	Pro	Cys
				260					265					270
Gln	Pro	Ser	Leu	Gly	His	Gly	Pro	Trp	Ala	Asp	Val	Lys	Glu	Pro
				275					280					285
Ser	Ser	Ser	Gly	Gly	Gly	Gln	Leu	Gly	Arg	Ala	Ser	Leu	Leu	Gly
				290					295					300
Leu	Gly	Lys	Leu	Tyr	Leu	Leu								
				305										

<210> 70
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:336120.1.orf1:2000MAY01

Ile	Ile	Pro	Gln	Arg	Ser	Asn	Gly	Asp	Arg	Trp	Gly	Arg	Ser	Leu
	1			5					10					15
Leu	Pro	Ser	Arg	Thr	Phe	Leu	Gln	Ala	Leu	Asn	Leu	Gly	Ile	Glu
				20					25					30
Val	Ile	Asn	Thr	Thr	Asp	Tyr	Leu	His	Phe	Ser	Lys	Glu	Cys	Ser
				35					40					45
Arg	Ala	Leu	Leu	Lys	Met	Gln	Tyr	Cys	Pro	His	Cys	Gln	Gly	Leu
				50					55					60
Ala	Leu	Thr	Lys	Pro	Cys	Met	Gly	Tyr	Cys	Leu	Asn	Val	Met	Arg
				65					70					75
Gly	Cys	Leu	Ala	His	Met	Ala	Glu	Leu	Asn	Pro	His	Trp	His	Ala
				80					85					90
Tyr	Ile	Arg	Ser	Leu	Glu	Glu	Leu	Ser	Asp	Ala	Met	His	Gly	Thr
				95					100					105
Tyr	Asp	Ile	Gly	His	Val	Leu	Leu	Asn	Phe	His	Leu	Leu	Val	Asn
				110					115					120
Asp	Ala	Val	Leu	Gln	Ala	His	Leu	Asn	Gly	Gln	Lys	Leu	Leu	Glu
				125					130					135
Gln	Val	Asn	Arg	Ile	Cys	Gly	Arg	Pro	Val	Arg	Thr	Pro	Thr	Gln
				140					145					150
Ser	Pro	Arg	Cys	Ser	Phe	Asp	Gln	Ser	Lys	Glu	Lys	His	Gly	Met

				155					160					165
Lys	Thr	Thr	Thr	Arg	Asn	Ser	Glu	Glu	Thr	Leu	Ala	Asn	Arg	Arg
				170					175					180
Lys	Glu	Phe	Ile	Asn	Ser	Leu	Ser	Thr	Val	Gln	Val	Ile	Leu	Trp
				185					190					195
Arg	Ser	Ser												

<210> 71
 <211> 227
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:234104.2.orf1:2000MAY01

<400> 71

Ala	Thr	Pro	Ser	Gly	Arg	Pro	Gln	Ser	Trp	Thr	Arg	Phe	Ser	Leu
1				5					10					15
Trp	Arg	Gly	Pro	Arg	Arg	Thr	Arg	Pro	Ser	Pro	Pro	Ala	Pro	Ala
				20					25					30
Pro	Ala	Gly	Met	Gly	Ser	Glu	His	Asp	Gly	Arg	Ser	Gly	Pro	Val
				35					40					45
Leu	Thr	Pro	Ala	Asp	Thr	Leu	His	Pro	Pro	Thr	Arg	Leu	Gln	Pro
				50					55					60
Ser	Pro	Pro	Asp	Thr	His	Pro	Gly	Gly	Ser	Ser	Leu	Pro	Ala	Pro
				65					70					75
Arg	Pro	Ala	Leu	Ser	Cys	Trp	Ala	Arg	Val	Phe	Ala	Ser	Leu	Val
				80					85					90
Arg	Pro	Ala	Gly	Phe	Pro	Gly	Gly	Thr	His	Gly	Ala	Pro	Gly	Met
				95					100					105
Pro	Leu	Gly	Ser	Pro	Ser	Thr	Ser	Thr	Ala	Gln	Trp	Pro	Tyr	Val
				110					115					120
Gln	Leu	Val	Pro	Gly	Pro	Arg	Val	Arg	Lys	Thr	Ala	Ser	Arg	Ser
				125					130					135
His	Cys	Gln	Glu	Arg	Ala	Glu	Glu	Trp	Ser	Gly	Pro	Arg	Arg	Pro
				140					145					150
Trp	Gly	Glu	Gly	Asp	Pro	Gly	Pro	Val	Thr	Ala	Thr	Pro	Gly	Thr
				155					160					165
Pro	Gly	Gly	Ala	Pro	Thr	Ser	Ala	Phe	Ser	Cys	Ala	Ala	Lys	Leu
				170					175					180
Gln	Lys	Pro	Asp	Ala	Gly	Leu	Val	Val	Ala	Asn	Gly	Thr	Met	Cys
				185					190					195
Cys	Pro	Ala	Lys	His	Thr	Trp	Arg	Ser	Gly	Pro	Lys	Ile	Pro	Ile
				200					205					210
Leu	Asp	Phe	His	Pro	Ala	Pro	Ser	Ser	Thr	Pro	Arg	Ser	Ala	Leu
				215					220					225
Ser	His													

<210> 72
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:450887.1.orf3:2000MAY01

<400> 72

Ser	Val	His	Phe	Ser	Arg	Lys	Gly	Phe	Val	Leu	Met	Ala	Pro	Pro
1				5					10					15
Gln	Pro	Lys	Ser	Gly	Leu	Phe	Val	Gly	Ile	Asn	Lys	Gly	His	Val
				20					25					30
Val	Thr	Lys	Arg	Glu	Leu	Pro	Pro	Arg	Pro	Cys	His	Arg	Lys	Gly
				35					40					45

Lys Ser Thr Lys Arg Val Ser Met Val Arg Gly Leu Ile Arg Glu
 50 55 60
 Val Ala Gly Phe Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu
 65 70 75
 Lys Val Gly Lys Asp Lys Arg Ala Leu Lys Leu Ala Lys Arg Lys
 80 85 90
 Leu Gly Thr His Lys Arg Ala Lys Lys Lys Arg Glu Glu Met Ala
 95 100 105
 Gly Val Leu Arg Lys Met Arg Ser Ala Gly Thr His Thr Asp Lys
 110 115 120
 Lys Lys

<210> 73
 <211> 209
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:119992.3.orf2:2000MAY01

<400> 73
 Cys Ser Gln Ile Glu Leu Ala Ile Glu Leu Asp Ser Thr His Leu
 1 5 10 15
 Val Thr Leu Gly Gly Val Leu Arg Gln Gln Leu Val Val Ser Lys
 20 25 30
 Glu Leu Arg Met Tyr Asp Glu Arg Ala Gln Glu Trp Arg Ser Leu
 35 40 45
 Ala Pro Met Asp Ala Pro Arg Tyr Gln His Gly Tyr Trp Leu Phe
 50 55 60
 Ile Gly Asn Phe Leu Tyr Val Val Gly Gly Gln Ser Asn Tyr Asp
 65 70 75
 Thr Lys Gly Lys Thr Ala Val Asp Thr Val Phe Arg Phe Asp Pro
 80 85 90
 Arg Tyr Asn Lys Trp Met Gln Val Ala Ser Leu Asn Glu Lys Arg
 95 100 105
 Thr Phe Phe His Leu Ser Ala Leu Lys Gly His Leu Tyr Ala Val
 110 115 120
 Gly Gly Arg Ser Ala Ala Gly Glu Leu Gly Thr Val Glu Cys Tyr
 125 130 135
 Asn Pro Arg Met Asn Glu Trp Ser Tyr Val Ala Lys Met Ser Glu
 140 145 150
 Pro His Tyr Gly His Ala Gly Thr Val Tyr Gly Gly Leu Met Tyr
 155 160 165
 Ile Ser Gly Gly Ile Thr His Asp Thr Phe Gln Asn Glu Leu Met
 170 175 180
 Cys Phe Asp Pro Asp Thr Asp Lys Trp Met Gln Lys Ala Pro Met
 185 190 195
 Thr Thr Val Arg Gly Leu His Cys Met Cys Thr Arg Trp Arg
 200 205

<210> 74
 <211> 312
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:197241.2.orf1:2000MAY01

<400> 74
 Tyr Ser Arg Ile Leu Ile Leu Gln Met Phe Ile Leu Gly Ala Ile
 1 5 10 15
 Ile Gln Ile Leu Pro Trp Val Met Ala Ser Gln Asn Ser Lys His
 20 25 30
 His Pro Glu Leu Val Asp Leu Phe Ser Arg Ser Gly Ile Tyr Ile

				35					40					45
Lys	Gln	Val	Val	Leu	Cys	Lys	Phe	His	Ser	Val	Phe	Leu	Ser	Gln
				50					55					60
Lys	Gly	Gln	Val	Tyr	Thr	Cys	Gly	His	Gly	Pro	Gly	Arg	Ala	Ile
				65					70					75
Arg	Asp	Met	Gly	Asp	Glu	Gln	Thr	Cys	Leu	Val	Pro	Arg	Leu	Val
				80					85					90
Glu	Gly	Leu	Asn	Gly	His	Asn	Cys	Ser	Gln	Val	Ala	Ala	Ala	Lys
				95					100					105
Asp	His	Thr	Val	Val	Leu	Thr	Glu	Asp	Gly	Cys	Val	Tyr	Thr	Phe
				110					115					120
Gly	Leu	Asn	Ile	Phe	His	Gln	Leu	Gly	Ile	Ile	Pro	Pro	Pro	Ser
				125					130					135
Ser	Cys	Asn	Val	Pro	Arg	Gln	Ile	Gln	Ala	Lys	Tyr	Leu	Lys	Gly
				140					145					150
Arg	Thr	Ile	Ile	Gly	Val	Ala	Ala	Gly	Arg	Phe	His	Thr	Val	Leu
				155					160					165
Trp	Thr	Arg	Glu	Ala	Val	Tyr	Thr	Met	Gly	Leu	His	Gly	Gly	Gln
				170					175					180
Leu	Gly	Cys	Leu	Leu	Asp	Pro	Asn	Gly	Glu	Lys	Cys	Val	Thr	Ala
				185					190					195
Pro	Arg	Gln	Val	Ser	Ala	Leu	His	His	Lys	Asp	Ile	Ala	Leu	Ser
				200					205					210
Leu	Val	Ala	Ala	Ser	Asp	Gly	Ala	Thr	Val	Cys	Val	Thr	Thr	Arg
				215					220					225
Gly	Asp	Ile	Tyr	Leu	Leu	Ala	Asp	Tyr	Gln	Cys	Lys	Lys	Met	Ala
				230					235					240
Ser	Lys	Gln	Leu	Asn	Leu	Lys	Lys	Val	Leu	Val	Ser	Gly	Gly	His
				245					250					255
Met	Glu	Tyr	Lys	Val	Asp	Pro	Glu	His	Leu	Lys	Glu	Asn	Gly	Gly
				260					265					270
Gln	Lys	Ile	Cys	Ile	Leu	Ala	Met	Asp	Gly	Ala	Gly	Arg	Val	Phe
				275					280					285
Cys	Trp	Arg	Ser	Val	Asn	Ser	Ser	Leu	Lys	Gln	Cys	Arg	Leu	Gly
				290					295					300
Leu	Ser	Thr	Ser	Gly	Ser	Ser	Phe	Leu	Ile	Trp	Leu			
				305					310					

<210> 75
 <211> 190
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:406860.20.orf3:2000MAY01

<400>	75													
Leu	Tyr	Val	Met	Leu	Glu	Met	Thr	Arg	Pro	Ser	Ser	Leu	Ser	Leu
	1			5					10					15
Ser	Gln	Leu	Ala	Leu	Phe	Ser	Arg	Ala	Val	Leu	Pro	Val	Gly	Arg
				20					25					30
Ala	Glu	Asp	Leu	Ala	Gly	Glu	Ala	Gly	Glu	Ala	Cys	Trp	Pro	Ser
				35					40					45
Leu	Cys	Ala	Pro	Leu	His	Ala	His	Pro	Pro	Ala	Pro	Pro	Glu	Arg
				50					55					60
Ile	Val	His	Pro	Ala	Ala	Arg	Ser	Leu	Asp	Leu	His	Phe	Gly	Ala
				65					70					75
Pro	Gly	Arg	Val	Glu	Leu	Arg	Cys	Glu	Val	Ala	Pro	Ala	Gly	Ser
				80					85					90
Gln	Val	Arg	Trp	Tyr	Lys	Asp	Gly	Leu	Glu	Val	Glu	Ala	Ser	Asp
				95					100					105
Ala	Leu	Gln	Leu	Gly	Ala	Glu	Gly	Pro	Thr	Arg	Thr	Leu	Thr	Leu
				110					115					120
Pro	His	Ala	Gln	Pro	Glu	Asp	Ala	Gly	Glu	Tyr	Val	Cys	Glu	Thr
				125					130					135
Arg	His	Glu	Ala	Ile	Thr	Phe	Asn	Val	Ile	Leu	Ala	Glu	Pro	Pro


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140                               145                               150
Val Gln Phe Leu Ala Leu Glu Thr Thr Pro Ser Pro Leu Cys Val
155                               160                               165
Gly Pro Gly Glu Pro Val Val Gln Glu Gly Glu Gly Leu Glu Leu
170                               175                               180
His Ala Glu Gly Pro Ala Glu Ser Leu His
185                               190

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<210> 76
 <211> 295
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:142384.1.orf3:2000MAY01

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<400> 76
Arg Thr Cys Cys Arg Val Val Pro Glu Ala Lys Gln Arg Trp Arg
 1                               5                               10                               15
Arg Val Arg Leu Arg Arg Arg Gln Arg Arg Ala Pro Gly Arg Arg
20                               25                               30
Ala Pro Gly Arg Ala Ala Leu Leu Val Leu Leu Ala Leu Ala Ala
35                               40                               45
Ala Ala Ala Gly Ser Gly Arg Leu Ser Cys Arg Met Cys Gly Arg
50                               55                               60
Arg Arg Arg Ser Val Gly Gly Ala Gly Gly Pro Gly Ser Gly Leu
65                               70                               75
Ala Pro Leu Pro Gly Leu Pro Pro Ser Ala Ala Ala His Gly Ala
80                               85                               90
Ala Leu Leu Ser His Trp Asp Pro Thr Leu Ser Ser Asp Trp Asp
95                               100                              105
Gly Glu Arg Thr Ala Pro Gln Cys Leu Leu Arg Ile Lys Arg Asp
110                              115                              120
Ile Met Ser Ile Tyr Lys Glu Pro Pro Pro Gly Met Phe Val Val
125                              130                              135
Pro Asp Thr Val Asp Met Thr Lys Ile His Ala Leu Ile Thr Gly
140                              145                              150
Pro Phe Asp Thr Pro Tyr Glu Gly Gly Phe Phe Leu Phe Val Phe
155                              160                              165
Arg Cys Pro Pro Asp Tyr Pro Ile His Pro Pro Arg Val Lys Leu
170                              175                              180
Met Thr Thr Gly Asn Asn Thr Val Arg Phe Asn Pro Asn Phe Tyr
185                              190                              195
Arg Asn Gly Lys Val Cys Leu Ser Ile Leu Gly Thr Trp Thr Gly
200                              205                              210
Pro Ala Trp Ser Pro Ala Gln Ser Ile Ser Ser Val Leu Ile Ser
215                              220                              225
Ile Gln Ser Leu Met Thr Glu Asn Pro Tyr His Asn Glu Pro Gly
230                              235                              240
Phe Glu Gln Glu Arg His Pro Gly Asp Ser Lys Asn Tyr Asn Glu
245                              250                              255
Cys Ile Arg His Glu Thr Ile Arg Val Ala Val Cys Asp Met Met
260                              265                              270
Glu Gly Lys Cys Pro Cys Pro Glu Pro Leu Arg Gly Val Met Glu
275                              280                              285
Lys Ser Phe Leu Glu Tyr Tyr Asp Phe Tyr
290                              295

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<210> 77
 <211> 288
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:895427.1.orf2:2000MAY01

<400> 77
 Ala Pro Arg Leu Trp Ala Cys Pro Cys His Cys Trp Trp Ser Gly
 1 5 10 15
 Ser Gly Pro Pro Ala Arg Cys Pro Tyr Ile Ile Gln Lys Cys Val
 20 25 30
 Gly Gln Ile Glu Arg Arg Gly Leu Arg Val Val Gly Leu Tyr Arg
 35 40 45
 Leu Cys Gly Ser Ala Ala Val Lys Lys Glu Leu Arg Asp Ala Phe
 50 55 60
 Glu Arg Asp Ser Ala Ala Val Cys Leu Ser Glu Asp Leu Tyr Pro
 65 70 75
 Asp Ile Asn Val Ile Thr Gly Ile Leu Lys Asp Tyr Leu Arg Glu
 80 85 90
 Leu Pro Thr Pro Leu Ile Thr Gln Pro Leu Tyr Lys Val Val Leu
 95 100 105
 Glu Ala Met Ala Pro Gly Thr Pro Gln Thr Glu Phe Pro Pro Pro
 110 115 120
 Leu Arg Ala Pro Glu Gly Ser Tyr Ser Cys Leu Pro Asp Val Glu
 125 130 135
 Arg Ala Thr Leu Thr Leu Leu Leu Asp His Leu Arg Leu Val Ser
 140 145 150
 Ser Phe His Ala Tyr Asn Arg Met Thr Pro Gln Asn Leu Ala Val
 155 160 165
 Cys Phe Gly Pro Val Leu Leu Pro Ala Arg Gln Ala Pro Thr Arg
 170 175 180
 Pro Arg Ala Arg Ser Ser Gly Pro Gly Leu Ala Ser Ala Val Asp
 185 190 195
 Phe Lys His His Ile Glu Val Leu His Tyr Leu Leu Gln Ser Trp
 200 205 210
 Pro Asp Pro Arg Leu Pro Arg Gln Ser Pro Asp Val Ala Pro Tyr
 215 220 225
 Leu Arg Pro Lys Arg Gln Pro Pro Leu His Leu Pro Leu Ala Asp
 230 235 240
 Pro Glu Val Val Thr Arg Pro Arg Gly Arg Gly Gly Pro Glu Ser
 245 250 255
 Pro Pro Ser Asn Arg Tyr Ala Gly Asp Trp Ser Val Cys Gly Arg
 260 265 270
 Gly Leu Pro Asp Leu Trp Ala Gly Phe Pro Val Arg Ala Arg Leu
 275 280 285
 Arg Pro Leu

<210> 78
 <211> 294
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:757439.1.orf1:2000MAY01

<400> 78
 Leu Ala Ala Pro Gln Ser His Ser Ile Pro Ser Pro Pro Gly Ala
 1 5 10 15
 His Leu Leu Lys Thr Arg Val Leu Pro Ser Ala Arg Arg Ala Arg
 20 25 30
 Ala Arg Gly Ala Arg Glu Leu Arg Ser Ala Arg Ala Met Gly Pro
 35 40 45
 Pro Pro Gly Ala Gly Val Ser Cys Arg Gly Gly Cys Gly Phe Ser
 50 55 60
 Arg Leu Leu Ala Trp Cys Phe Leu Leu Ala Leu Ser Pro Gln Ala
 65 70 75
 Pro Gly Ser Arg Gly Ala Glu Ala Val Trp Thr Ala Tyr Leu Asn
 80 85 90
 Val Ser Trp Arg Val Pro His Thr Gly Val Asn Arg Thr Val Trp
 95 100 105
 Glu Leu Ser Glu Glu Gly Val Tyr Gly Pro Asp Ser Pro Leu Glu

Pro Val Ala Gly	110	115	120
Val Leu Val Pro Pro	125	130	135
Asn Ala Cys Asn	140	145	150
Gly Ser Thr Val	155	160	165
Gly Gly Cys Thr	170	175	180
Gly Ala Ser Gly	185	190	195
Glu Val Ile Pro	200	205	210
Ile Met Ile Arg	215	220	225
Ser Lys Arg His	230	235	240
Thr Trp Pro Leu	245	250	255
Cys Pro Phe Leu	260	265	270
Phe Tyr Ser Ala	275	280	285
Lys Gln Arg Pro	290		

<210> 79
 <211> 196
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:1144066.1.orf3:2000MAY01

<400> 79

Gly Ala Thr Pro Arg	5	10	15
Arg Ala Ala His Ala	20	25	30
Arg Pro Val Gln Ile	35	40	45
Arg Lys Leu Ala Ile	50	55	60
Met Gly Ser Glu Asp	65	70	75
Met Thr Phe Arg Pro	80	85	90
Tyr Val Gly Tyr Ile	95	100	105
Gly Lys Ile Ile Pro	110	115	120
Asp Asp Ile Asp Asp	125	130	135
Val Thr Gly Gln Ser	140	145	150
Lys Gly Met Thr Val	155	160	165
Lys Tyr Cys Thr Pro	170	175	180
Lys Tyr Trp Glu Gly	185	190	195

Gly

<210> 80
 <211> 745

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: LI:243660.4.orf3:2000MAY01

<400> 80

Glu	Gly	Trp	Thr	Gln	Pro	Gln	Gln	Ala	Gly	Glu	Gly	Pro	His	Pro
1				5					10					15
Ala	Ala	His	Glu	Cys	Leu	His	Asp	Leu	Gln	Gln	Ala	Ala	Pro	Gly
				20					25					30
Pro	Gly	Pro	Pro	Ala	Ser	Ser	Gln	Pro	Gly	Gln	Pro	Asp	Arg	Gln
				35					40					45
Gln	Asp	Pro	Gly	Arg	Val	Val	Val	Cys	Pro	Gly	Ala	Gln	Gly	Glu
				50					55					60
Ala	Glu	Val	Pro	Arg	Pro	Gly	Leu	Pro	Gly	Glu	Gly	Gly	Pro	Leu
				65					70					75
Gln	Gly	Pro	Pro	Ser	Ile	Gly	Ser	Gly	Ala	Thr	Arg	Thr	Glu	Arg
				80					85					90
Ser	Pro	Ala	Gln	Arg	Pro	Ser	Pro	Arg	Ser	Leu	Gly	Leu	Ala	Gly
				95					100					105
Gly	His	Lys	Glu	Thr	Arg	Glu	Arg	Ser	Met	Ser	Glu	Thr	Gly	Thr
				110					115					120
Ala	Ala	Cys	Pro	Trp	Val	Cys	Pro	Arg	Glu	Leu	Leu	Ser	Val	Ala
				125					130					135
Ala	Gln	Thr	Leu	Leu	Ser	Ser	Asp	Thr	Lys	Ala	Pro	Gly	Ser	Ser
				140					145					150
Ser	Cys	Gly	Ala	Glu	Arg	Leu	His	Thr	Val	Gly	Gly	Pro	Gly	Ser
				155					160					165
Ala	Arg	Pro	Arg	Ala	Phe	Ser	His	Ser	Gly	Val	His	Ser	Leu	Asp
				170					175					180
Gly	Gly	Glu	Val	Asp	Ser	Gln	Ala	Leu	Gln	Glu	Leu	Thr	Gln	Met
				185					190					195
Val	Ser	Gly	Pro	Ala	Ser	Tyr	Ser	Gly	Pro	Lys	Pro	Ser	Thr	Gln
				200					205					210
Tyr	Gly	Ala	Pro	Gly	Pro	Phe	Ala	Ala	Pro	Gly	Glu	Gly	Gly	Ala
				215					220					225
Leu	Ala	Ala	Thr	Gly	Arg	Pro	Pro	Leu	Leu	Pro	Thr	Arg	Ala	Ser
				230					235					240
Arg	Ser	Gln	Arg	Ala	Ala	Ser	Glu	Asp	Met	Thr	Ser	Asp	Glu	Glu
				245					250					255
Arg	Met	Val	Ile	Cys	Glu	Glu	Glu	Gly	Asp	Asp	Asp	Val	Ile	Ala
				260					265					270
Asp	Asp	Gly	Phe	Gly	Pro	Thr	Asp	Leu	Asp	Leu	Lys	Cys	Lys	Glu
				275					280					285
Arg	Val	Thr	Asp	Ser	Glu	Ser	Gly	Asp	Ser	Ser	Gly	Glu	Asp	Pro
				290					295					300
Glu	Gly	Asn	Lys	Gly	Phe	Gly	Arg	Lys	Val	Phe	Ser	Pro	Val	Ile
				305					310					315
Arg	Ser	Ser	Phe	Thr	His	Cys	Arg	Pro	Pro	Leu	Asp	Pro	Glu	Pro
				320					325					330
Pro	Gly	Pro	Pro	Asp	Pro	Pro	Val	Ala	Phe	Gly	Lys	Gly	Tyr	Gly
				335					340					345
Ser	Ala	Pro	Ser	Ser	Ser	Ala	Ser	Ser	Pro	Ala	Ser	Ser	Ser	Ala
				350					355					360
Ser	Ala	Ala	Thr	Ser	Phe	Ser	Leu	Gly	Ser	Gly	Thr	Phe	Lys	Ala
				365					370					375
Gln	Glu	Ser	Gly	Gln	Gly	Ser	Thr	Ala	Gly	Pro	Leu	Arg	Pro	Pro
				380					385					390
Pro	Pro	Gly	Ala	Gly	Gly	Pro	Ala	Thr	Pro	Ser	Lys	Ala	Thr	Arg
				395					400					405
Phe	Leu	Pro	Met	Asp	Pro	Ala	Thr	Phe	Arg	Arg	Lys	Arg	Pro	Glu
				410					415					420
Ser	Val	Gly	Gly	Leu	Glu	Pro	Pro	Gly	Pro	Ser	Val	Ile	Ala	Ala
				425					430					435
Pro	Pro	Ser	Gly	Gly	Gly	Asn	Ile	Leu	Gln	Thr	Leu	Val	Leu	Pro

Pro Asn Lys Glu	440	Glu Gln Glu Gly Gly	445	Gly Ala Arg Val Pro	450
Ala Pro Ala Pro	455	Ser Leu Ala Tyr Gly	460	Ala Pro Ala Ala Pro	465
Ser Arg Pro Ala	470	Ala Thr Met Val Thr	475	Asn Val Val Arg Pro	480
Ser Ser Thr Pro	485	Val Pro Ile Ala Ser	490	Lys Pro Phe Pro Thr	495
Gly Arg Ala Glu	500	Ala Ser Pro Asn Asp	505	Thr Ala Gly Ala Arg	510
Glu Met Gly Thr	515	Gly Ser Arg Val Pro	520	Gly Gly Ser Pro Leu	525
Val Ser Leu Val	530	Tyr Ser Asp Lys Lys	535	Ser Ala Ala Ala Thr	540
Pro Ala Pro His	545	Leu Val Ala Gly Pro	550	Leu Leu Gly Thr Val	555
Lys Ala Pro Ala	560	Thr Val Thr Asn Leu	565	Leu Val Gly Thr Pro	570
Tyr Gly Ala Pro	575	Ala Pro Pro Ala Val	580	Gln Phe Ile Ala Gln	585
Ala Pro Gly Gly	590	Gly Thr Thr Ala Gly	595	Ser Gly Ala Gly Ala	600
Ser Gly Pro Asn	605	Gly Thr Thr Ala Gly	610	Ser Gly Ala Gly Ala	615
Ala Leu Gly Lys	620	Gly Pro Val Pro Leu	625	Gly Ile Leu Gln Pro	630
Pro Thr Leu Pro	635	Ala Gly Gly Ile Thr	640	Gln Val Gln Tyr Ile	645
Ala Pro Gly Thr	650	Gln Gln Leu Gln Val	655	Ala Pro Ala Pro Ala	660
His Gln His Pro	665	Lys Ala Ala Ala Pro	670	Met Arg Pro Cys Thr	675
Gln Ser Pro Gly	680	Phe His Pro Pro Thr	685	Gly His Phe His Gln	690
Ala Val Cys Thr	695	Cys His Cys Thr His	700	Ser Trp His Pro His	705
Ser Arg Ala Gly	710	Leu Arg Pro Thr Pro	715	Gln Ser Pro Val Ser	720
Trp Glu Gly Pro	725	Pro Ala Pro Gly Trp	730	Leu Ser Pro Ala Ala	735
	740	Ser Ala Ser Gly Arg	745	Pro	

<210> 81
 <211> 256
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:334386.1.orf3:2000MAY01

<400> 81
 Leu Ala Met Lys Asp Met Leu Thr Val Val Asp Leu Leu Leu Glu
 1 5 10 15
 Gly Gly Ala Asp Val Asp His Thr Asp Asn Asn Gly Arg Thr Pro
 20 25 30
 Leu Leu Ala Ala Ala Ser Met Gly His Ala Ser Val Val Asn Thr
 35 40 45
 Leu Leu Phe Trp Gly Ala Ala Val Asp Ser Ile Asp Ser Glu Gly
 50 55 60
 Arg Thr Val Leu Ser Ile Ala Ser Ala Gln Gly Asn Val Glu Val
 65 70 75
 Val Arg Thr Leu Leu Asp Arg Gly Leu Asp Glu Asn His Arg Asp
 80 85 90
 Asp Ala Gly Trp Thr Pro Leu His Met Ala Ala Phe Glu Gly His
 95 100 105
 Arg Leu Ile Cys Glu Ala Leu Ile Glu Gln Gly Ala Arg Thr Asn

	110		115		120
Glu Ile Asp Asn Asp Gly Arg Ile Pro Phe Ile Leu Ala Ser Gln					
	125		130		135
Glu Gly His Tyr Asp Cys Val Gln Ile Leu Leu Glu Asn Lys Ser					
	140		145		150
Asn Ile Asp Gln Arg Gly Tyr Asp Gly Arg Asn Ala Leu Arg Val					
	155		160		165
Ala Ala Leu Glu Gly His Arg Asp Ile Val Glu Leu Leu Phe Ser					
	170		175		180
His Gly Ala Asp Val Asn Cys Lys Asp Ala Asp Gly Arg Pro Thr					
	185		190		195
Leu Tyr Ile Leu Ala Leu Glu Asn Gln Leu Thr Met Ala Glu Tyr					
	200		205		210
Phe Leu Glu Asn Gly Ala Asn Val Glu Ala Ser Asp Ala Glu Gly					
	215		220		225
Arg Thr Ala Leu His Val Ser Cys Trp Gln Gly His Met Gly Asn					
	230		235		240
Gly Ala Gly Pro Asp Ser Ile Pro Cys Arg Arg Gln Cys Cys Arg					
	245		250		255
Gln					

<210> 82
 <211> 235
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:347572.1.orf1:2000MAY01

<400> 82	
Met Pro Ile Leu Pro Ile Ser Val Gln Leu Asp Ala Ser Leu Leu	
1 5 10 15	
Ile Cys Leu Val Ile Cys Ala Gly Arg Phe Trp Thr Asn Leu Tyr	
20 25 30	
Ser Leu Thr Val Pro Phe Gly Gln Lys Pro Asn Ile Asp Val Thr	
35 40 45	
Asp Ala Met Val Asp Gln Ala Trp Asp Ala Gln Arg Ile Phe Lys	
50 55 60	
Glu Ser Ala Glu Leu Leu Cys Ile Cys Trp Ser Ser Leu Tyr Asp	
65 70 75	
Ser Arg Ile Leu Arg Gln Ile Pro Cys Tyr Thr Asp Pro Gly Asn	
80 85 90	
Val Gln Lys Ala Leu Cys His Pro His Ser Leu Gly Pro Gly Glu	
95 100 105	
Gly Arg Leu Gln Arg Ser Leu Cys Ala Gln Arg Val Thr Met Asp	
110 115 120	
Asp Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp	
125 130 135	
Met Ala Tyr Ala Gly Gln Pro Phe Ser Ala Lys Glu Met Glu Leu	
140 145 150	
Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile Met Ser Leu Ser	
155 160 165	
Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu Leu Ser Pro	
170 175 180	
Glu Phe Ser Thr Asn Asp Asn Glu Thr Glu Ile Asn Phe Leu Leu	
185 190 195	
Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe Thr Tyr Met	
200 205 210	
Leu Glu Lys Trp Arg Trp Met Val Phe Lys Arg Gly Asn Ser Gln	
215 220 225	
Arg Pro Val Gly Glu Lys Gly Gly Gly Arg	
230 235	

<210> 83
 <211> 617

<212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:817314.1.orf1:2000MAY01

<400> 83
 Asn Met Ala Gln Phe Tyr Tyr Lys Arg Asn Val Asn Ala Pro Tyr
 1 5 10 15
 Arg Asp Arg Ile Pro Leu Arg Ile Val Arg Ala Glu Ser Glu Leu
 20 25 30
 Ser Pro Ser Glu Lys Ala Tyr Leu Asn Ala Val Glu Lys Gly Asp
 35 40 45
 Tyr Ala Ser Val Lys Lys Ser Leu Glu Glu Ala Glu Ile Tyr Phe
 50 55 60
 Lys Ile Asn Ile Asn Cys Ile Asp Pro Leu Gly Arg Thr Ala Leu
 65 70 75
 Leu Ile Ala Ile Glu Asn Glu Asn Leu Glu Leu Ile Glu Leu Leu
 80 85 90
 Leu Ser Phe Asn Val Tyr Val Gly Asp Ala Leu Leu His Ala Ile
 95 100 105
 Arg Lys Glu Val Val Gly Ala Val Glu Leu Leu Leu Asn His Lys
 110 115 120
 Lys Pro Ser Gly Glu Lys Gln Val Pro Pro Ile Leu Leu Asp Lys
 125 130 135
 Gln Phe Ser Glu Phe Thr Pro Asp Ile Thr Pro Ile Ile Leu Ala
 140 145 150
 Ala His Thr Asn Asn Tyr Glu Ile Ile Lys Leu Leu Val Gln Lys
 155 160 165
 Gly Val Ser Val Pro Arg Pro His Glu Val Arg Cys Asn Cys Val
 170 175 180
 Glu Cys Val Ser Ser Ser Asp Val Asp Ser Leu Arg His Ser Arg
 185 190 195
 Ser Arg Leu Asn Ile Tyr Lys Ala Leu Ala Ser Pro Ser Leu Ile
 200 205 210
 Ala Leu Ser Ser Glu Asp Pro Phe Leu Thr Ala Phe Gln Leu Ser
 215 220 225
 Trp Glu Leu Gln Glu Leu Ser Lys Val Glu Asn Glu Phe Lys Ser
 230 235 240
 Glu Tyr Glu Glu Leu Ser Arg Gln Cys Lys Gln Phe Ala Lys Asp
 245 250 255
 Leu Leu Asp Gln Thr Arg Ser Ser Arg Glu Leu Glu Ile Ile Leu
 260 265 270
 Asn Tyr Arg Asp Asp Asn Ser Leu Ile Glu Glu Gln Ser Gly Asn
 275 280 285
 Asp Leu Ala Arg Leu Lys Leu Ala Ile Lys Tyr Arg Gln Lys Glu
 290 295 300
 Phe Val Ala Gln Pro Asn Cys Gln Gln Leu Leu Ala Ser Arg Trp
 305 310 315
 Tyr Asp Glu Phe Pro Gly Trp Arg Arg Arg His Trp Ala Val Lys
 320 325 330
 Met Val Thr Cys Phe Ile Ile Gly Leu Leu Phe Pro Val Phe Ser
 335 340 345
 Val Cys Tyr Leu Ile Ala Pro Lys Ser Pro Leu Gly Leu Phe Ile
 350 355 360
 Arg Lys Pro Phe Ile Lys Phe Ile Cys His Thr Ala Ser Tyr Leu
 365 370 375
 Thr Phe Leu Phe Leu Leu Leu Ala Ser Gln His Ile Asp Arg
 380 385 390
 Ser Asp Leu Asn Arg Gln Gly Pro Pro Pro Thr Ile Val Glu Trp
 395 400 405
 Met Ile Leu Pro Trp Val Leu Gly Phe Ile Trp Gly Glu Ile Lys
 410 415 420
 Gln Met Trp Asp Gly Gly Leu Gln Asp Tyr Ile His Asp Trp Trp
 425 430 435
 Asn Leu Met Asp Phe Val Met Asn Ser Leu Tyr Leu Ala Thr Ile

	440		445		450
Ser Leu Lys Ile Val	Ala Phe Val Lys Tyr	Ser Ala Leu Asn Pro			
	455		460		465
Arg Glu Ser Trp Asp	Met Trp His Pro Thr	Leu Val Ala Glu Ala			
	470		475		480
Leu Phe Ala Ile Ala	Asn Ile Phe Ser Ser	Leu Arg Leu Ile Ser			
	485		490		495
Leu Phe Thr Ala Asn	Ser His Leu Gly Pro	Leu Gln Ile Ser Leu			
	500		505		510
Gly Arg Met Leu Leu	Asp Ile Leu Lys Phe	Leu Phe Ile Tyr Cys			
	515		520		525
Leu Val Leu Leu Ala	Phe Ala Asn Gly Leu	Asn Gln Leu Tyr Phe			
	530		535		540
Tyr Tyr Glu Glu Thr	Lys Gly Leu Thr Cys	Lys Gly Ile Arg Cys			
	545		550		555
Glu Lys Gln Asn Asn	Ala Phe Ser Thr Leu	Phe Glu Thr Leu Gln			
	560		565		570
Ser Leu Phe Trp Ser	Ile Phe Gly Leu Ile	Asn Leu Tyr Val Thr			
	575		580		585
Asn Val Lys Ala Gln	His Glu Phe Thr Glu	Phe Val Gly Ala Thr			
	590		595		600
Leu Phe Gly Asp Ile	Thr Met Ser Ser Leu	Trp Leu Phe Tyr Ser			
	605		610		615

Thr Cys

<210> 84
 <211> 293
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:000290.1.orf3:2000MAY01

<400> 84

Gly Ala His Ala Lys	Thr Gly Ile Gln Ile	Gly Met Leu Ser Thr		
1	5	10	15	
Gly Lys Asp Arg Ser	Leu Arg Val Thr Gly	Met Thr Trp Arg Ser		
	20	25	30	
Ser Tyr Val Pro Val	Ser Ala Pro Pro Pro	Asn Ser Ser Glu Gln		
	35	40	45	
Tyr Ser Ser Gly Ala	Gln Ser Ile Pro Ser	Thr Val Thr Val Ile		
	50	55	60	
Ala Pro Trp Ser Pro	Thr Leu Glu Asn Thr	Thr Trp Glu Leu Val		
	65	70	75	
Leu Leu Leu Leu Lys	Ile Ile Ser Ser Ser	Asn Ser Phe Gly Arg		
	80	85	90	
Asn Leu Pro Pro Lys	Arg Arg Cys Arg Asp	Tyr Asp Glu Arg Gly		
	95	100	105	
Phe Cys Val Leu Gly	Asp Leu Cys Gln Phe	Asp His Gly Asn Asp		
	110	115	120	
Pro Leu Val Val Asp	Glu Val Ala Leu Pro	Ser Met Ile Pro Phe		
	125	130	135	
Pro Pro Pro Pro Pro	Gly Leu Pro Pro Pro	Thr Thr Pro Gly Met		
	140	145	150	
Leu Met Pro Pro Met	Pro Gly Pro Gly Pro	Gly Pro Gly Pro Gly		
	155	160	165	
Pro Gly Pro Gly Pro	Gly Pro Gly Pro Gly	Pro Gly His Ser Met		
	170	175	180	
Arg Leu Pro Val Pro	Gln Gly His Gly Gln	Pro Pro Pro Ser Val		
	185	190	195	
Val Leu Pro Ile Pro	Arg Pro Pro Ile Thr	Gln Ser Ser Leu Ile		
	200	205	210	
Asn Ser Arg Asp Gln	Pro Gly Thr Ser Ala	Val Pro Asn Leu Ala		
	215	220	225	
Ser Val Gly Thr Arg	Leu Pro Pro Pro Leu	Pro Gln Asn Leu Leu		

Tyr	Thr	Val	Ser	230	Arg	Gln	Pro	Met	235	Tyr	Ser	Arg	Glu	His	Gly	240
				245					250							255
Ala	Ala	Ala	Ser	260	Glu	Arg	Leu	Gln	Leu	Gly	Thr	Pro	Pro	Pro	Leu	270
Leu	Ala	Ala	Arg	275	Leu	Val	Pro	Pro	Arg	Asn	Leu	Met	Gly	Ser	Ser	285
Ile	Gly	Tyr	His	290	Thr	Ser	Val	Ser		280						

<210> 85
 <211> 276
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:023518.3.orf3:2000MAY01

<400> 85

Leu	Ser	Pro	Asp	Arg	Leu	Leu	Val	Leu	Pro	Asp	Asn	Tyr	Ser	His
1				5					10					15
Phe	Ser	Gln	Ala	Ser	Ala	Asn	Leu	Gln	Gly	Pro	Ser	Arg	Thr	Thr
				20					25					30
Glu	Leu	Phe	His	Pro	Thr	Leu	Ala	Ser	Ile	Ser	Ser	Pro	Met	Leu
				35					40					45
Glu	Gly	Ala	Glu	Leu	Tyr	Phe	Asn	Val	Asp	His	Gly	Tyr	Leu	Glu
				50					55					60
Gly	Leu	Val	Arg	Gly	Cys	Lys	Ala	Ser	Leu	Leu	Thr	Gln	Gln	Asp
				65					70					75
Tyr	Ile	Asn	Leu	Val	Gln	Cys	Glu	Thr	Leu	Glu	Ala	Pro	Phe	Phe
				80					85					90
Gln	Asp	Cys	Met	Ser	Glu	Asn	Ala	Leu	Asp	Glu	Leu	Asn	Ile	Glu
				95					100					105
Leu	Leu	Arg	Asn	Lys	Leu	Tyr	Lys	Ser	Tyr	Leu	Glu	Ala	Phe	Tyr
				110					115					120
Lys	Phe	Cys	Lys	Asn	His	Gly	Asp	Val	Thr	Ala	Glu	Val	Met	Cys
				125					130					135
Pro	Ile	Leu	Glu	Phe	Glu	Ala	Asp	Arg	Arg	Ala	Phe	Ile	Ile	Thr
				140					145					150
Leu	Asn	Ser	Phe	Gly	Thr	Glu	Leu	Ser	Lys	Glu	Asp	Arg	Glu	Thr
				155					160					165
Leu	Tyr	Pro	Thr	Phe	Arg	Gln	Leu	Tyr	Pro	Glu	Gly	Leu	Arg	Leu
				170					175					180
Leu	Ala	Gln	Ala	Glu	Asp	Phe	Asp	Gln	Met	Lys	Asn	Val	Ala	Asp
				185					190					195
His	Tyr	Gly	Val	Tyr	Lys	Pro	Leu	Phe	Glu	Ala	Val	Gly	Gly	Ser
				200					205					210
Gly	Gly	Lys	Thr	Leu	Glu	Asp	Val	Phe	Tyr	Glu	Arg	Glu	Val	Gln
				215					220					225
Met	Asn	Val	Leu	Ala	Phe	Asn	Arg	Gln	Phe	His	Tyr	Gly	Val	Phe
				230					235					240
Tyr	Ala	Tyr	Val	Lys	Leu	Lys	Glu	Gln	Glu	Ile	Arg	Asn	Ile	Val
				245					250					255
Trp	Ile	Ala	Glu	Cys	Ile	Ser	Gln	Arg	His	Arg	Thr	Lys	Ile	Asn
				260					265					270
Ser	Tyr	Ile	Pro	Ile	Leu									
				275										

<210> 86
 <211> 355
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:1084246.1.orf3:2000MAY01

<400> 86
 Pro Leu Asp Arg Glu Thr Ser Thr Glu Tyr Asn Ile Thr Ile Ala
 1 5 10 15
 Val Thr Asp Leu Gly Thr Pro Arg Leu Lys Thr Gln Gln Asn Ile
 20 25 30
 Thr Val Gln Val Ser Asp Val Asn Asp Asn Ala Pro Ala Phe Thr
 35 40 45
 Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser Pro Ala
 50 55 60
 Leu His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser Gly Thr
 65 70 75
 Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp Pro His
 80 85 90
 Leu Pro Leu Ala Ser Leu Val Ser Ile Asn Ala Asp Asn Gly His
 95 100 105
 Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln Ala Phe
 110 115 120
 Glu Phe Arg Val Gly Ala Ser Asp Arg Gly Ser Pro Ala Leu Ser
 125 130 135
 Ser Glu Ala Leu Val Arg Val Leu Val Leu Asp Thr Asn Asp Asn
 140 145 150
 Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala Pro Cys
 155 160 165
 Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu Val Thr
 170 175 180
 Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala Trp Leu
 185 190 195
 Ser Tyr Gln Leu Leu Lys Ala Thr Glu Pro Gly Leu Phe Gly Val
 200 205 210
 Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu Ser Glu
 215 220 225
 Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys Asp Asn
 230 235 240
 Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val Leu Leu
 245 250 255
 Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu Ala Ala
 260 265 270
 Pro Ala Gln Ala Gln Ala Asp Ser Leu Thr Val Tyr Leu Val Val
 275 280 285
 Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val Leu Leu
 290 295 300
 Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala Ser Val
 305 310 315
 Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu Val
 320 325 330
 Asp Val Ser Gly Thr Gly Thr Leu Ser Gln Glu Leu Pro Val Arg
 335 340 345
 Gly Val Ser Asp Arg Arg Leu Trp Asp Trp
 350 355

<210> 87
 <211> 745
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:1165828.1.orf2:2000MAY01

<400> 87
 Val Phe Glu Met Leu Tyr Ser Ser Arg Gly Asp Pro Glu Gly Gln
 1 5 10 15
 Pro Leu Leu Leu Ser Leu Leu Ile Leu Ala Met Trp Val Val Gly
 20 25 30
 Ser Gly Gln Leu His Tyr Ser Val Pro Glu Glu Ala Glu His Gly
 35 40 45
 Thr Phe Val Gly Arg Ile Ala Gln Asp Leu Gly Leu Glu Leu Ala

				50					55					60
Glu	Leu	Val	Pro	Arg	Leu	Phe	Gln	Leu	Asp	Ser	Lys	Gly	Arg	Gly
				65					70					75
Asp	Leu	Leu	Glu	Val	Asn	Leu	Gln	Asn	Gly	Ile	Leu	Phe	Val	Asn
				80					85					90
Ser	Arg	Ile	Asp	Arg	Glu	Glu	Leu	Cys	Gly	Arg	Ser	Ala	Glu	Cys
				95					100					105
Ser	Ile	His	Leu	Glu	Val	Ile	Val	Asp	Arg	Pro	Leu	Gln	Val	Phe
				110					115					120
His	Val	Asp	Val	Glu	Val	Lys	Asp	Ile	Asn	Asp	Asn	Pro	Pro	Val
				125					130					135
Phe	Pro	Ala	Thr	Gln	Lys	Asn	Leu	Phe	Ile	Ala	Glu	Ser	Arg	Pro
				140					145					150
Leu	Asp	Ser	Arg	Phe	Pro	Leu	Glu	Gly	Ala	Ser	Asp	Ala	Asp	Ile
				155					160					165
Gly	Glu	Asn	Ala	Leu	Leu	Thr	Tyr	Arg	Leu	Ser	Pro	Asn	Glu	Tyr
				170					175					180
Phe	Phe	Leu	Asp	Val	Pro	Thr	Ser	Asn	Gln	Gln	Val	Lys	Pro	Leu
				185					190					195
Gly	Leu	Val	Leu	Arg	Lys	Leu	Leu	Asp	Arg	Glu	Glu	Thr	Pro	Glu
				200					205					210
Leu	His	Leu	Leu	Leu	Thr	Ala	Thr	Asp	Gly	Gly	Lys	Pro	Glu	Leu
				215					220					225
Thr	Gly	Thr	Val	Gln	Leu	Leu	Ile	Thr	Val	Leu	Asp	Asn	Asn	Asp
				230					235					240
Asn	Ala	Pro	Val	Phe	Asp	Arg	Thr	Leu	Tyr	Thr	Val	Lys	Leu	Pro
				245					250					255
Glu	Asn	Val	Ser	Ile	Gly	Thr	Leu	Val	Ile	His	Pro	Asn	Ala	Ser
				260					265					270
Asp	Leu	Asp	Glu	Gly	Leu	Asn	Gly	Asp	Ile	Ile	Tyr	Ser	Phe	Ser
				275					280					285
Ser	Asp	Val	Ser	Pro	Asp	Ile	Lys	Ser	Lys	Phe	His	Met	Asp	Pro
				290					295					300
Leu	Ser	Gly	Ala	Ile	Thr	Val	Ile	Gly	His	Met	Asp	Phe	Glu	Glu
				305					310					315
Ser	Arg	Ala	His	Lys	Ile	Pro	Val	Glu	Ala	Val	Asp	Lys	Gly	Phe
				320					325					330
Pro	Pro	Leu	Ala	Gly	His	Cys	Thr	Leu	Leu	Val	Glu	Val	Val	Asp
				335					340					345
Val	Asn	Asp	Asn	Ala	Pro	Gln	Leu	Thr	Ile	Lys	Thr	Leu	Ser	Val
				350					355					360
Pro	Val	Lys	Glu	Asp	Ala	Gln	Leu	Gly	Thr	Val	Ile	Ala	Leu	Ile
				365					370					375
Ser	Val	Ile	Asp	Leu	Asp	Ala	Asp	Ala	Asn	Gly	Gln	Val	Thr	Cys
				380					385					390
Ser	Leu	Thr	Pro	His	Val	Pro	Phe	Lys	Leu	Val	Ser	Thr	Tyr	Lys
				395					400					405
Asn	Tyr	Tyr	Ser	Leu	Val	Leu	Asp	Arg	Ala	Leu	Asp	Arg	Glu	Ser
				410					415					420
Val	Ser	Ala	Tyr	Glu	Leu	Val	Val	Thr	Ala	Arg	Asp	Gly	Gly	Ser
				425					430					435
Pro	Ser	Leu	Trp	Ala	Thr	Ala	Arg	Val	Ser	Val	Glu	Val	Ala	Asp
				440					445					450
Val	Asn	Asp	Asn	Ala	Pro	Ala	Phe	Ala	Gln	Ser	Glu	Tyr	Thr	Val
				455					460					465
Phe	Val	Lys	Glu	Asn	Asn	Pro	Pro	Gly	Cys	His	Ile	Phe	Thr	Val
				470					475					480
Ser	Ala	Arg	Asp	Ala	Asp	Ala	Gln	Glu	Asn	Ala	Leu	Val	Ser	Tyr
				485					490					495
Ser	Leu	Val	Glu	Arg	Arg	Leu	Gly	Glu	Arg	Ser	Leu	Ser	Ser	Tyr
				500					505					510
Val	Ser	Val	His	Ala	Glu	Ser	Gly	Lys	Val	Tyr	Ala	Leu	Gln	Pro
				515					520					525
Leu	Asp	His	Glu	Glu	Leu	Glu	Leu	Leu	Gln	Phe	Gln	Val	Ser	Ala
				530					535					540
Arg	Asp	Ala	Gly	Val	Pro	Pro	Leu	Gly	Ser	Asn	Val	Thr	Leu	Gln
				545					550					555

Val Phe Val Leu Asp Glu Asn Asp Asn Ala Pro Ala Leu Leu Thr
 560 565 570
 Pro Arg Met Arg Gly Thr Asp Gly Ala Val Ser Glu Met Val Leu
 575 580 585
 Arg Ser Val Gly Ala Gly Val Val Val Gly Lys Val Arg Ala Val
 590 595 600
 Asp Ala Asp Ser Gly Tyr Asn Ala Trp Leu Ser Tyr Glu Leu Gln
 605 610 615
 Pro Glu Thr Ala Ser Ala Ser Ile Pro Phe Arg Val Gly Leu Tyr
 620 625 630
 Thr Gly Glu Ile Ser Thr Thr Arg Ala Leu Asp Glu Thr Asp Ala
 635 640 645
 Pro Arg Gln Arg Leu Leu Val Leu Val Lys Asp His Gly Glu Pro
 650 655 660
 Ala Leu Thr Ala Thr Ala Thr Val Leu Val Ser Leu Val Glu Ser
 665 670 675
 Gly Gln Ala Pro Lys Ser Ser Ser Arg Ala Ser Val Gly Ala Thr
 680 685 690
 Gly Pro Glu Val Thr Leu Val Asp Val Asn Val Tyr Leu Ile Ile
 695 700 705
 Ala Ile Cys Ala Val Ser Ser Leu Leu Val Leu Thr Leu Leu Leu
 710 715 720
 Tyr Thr Val Leu Arg Cys Ser Ala Met Pro Thr Glu Gly Glu Cys
 725 730 735
 Ala Pro Gly Lys Ala Asp Ala Gly Val Phe
 740 745

<210> 88
 <211> 781
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:007302.1.orf2:2000MAY01

<400> 88
 Asp Ser His Cys Asn Ile Met Thr Lys Asp Lys Glu Pro Ile Val
 1 5 10 15
 Lys Ser Phe His Phe Val Cys Leu Met Ile Ile Ile Val Gly Thr
 20 25 30
 Arg Ile Gln Phe Ser Asp Gly Asn Glu Phe Ala Val Asp Lys Ser
 35 40 45
 Lys Arg Gly Leu Ile His Val Pro Lys Asp Leu Pro Leu Lys Thr
 50 55 60
 Lys Val Leu Asp Met Ser Gln Asn Tyr Ile Ala Glu Leu Gln Val
 65 70 75
 Ser Asp Met Ser Phe Leu Ser Glu Leu Thr Val Leu Arg Leu Ser
 80 85 90
 His Asn Arg Ile Gln Leu Leu Asp Leu Ser Val Phe Lys Phe Asn
 95 100 105
 Gln Asp Leu Glu Tyr Leu Asp Leu Ser His Asn Gln Leu Gln Lys
 110 115 120
 Ile Ser Cys His Pro Ile Val Ser Phe Arg His Leu Asp Leu Ser
 125 130 135
 Phe Asn Asp Phe Lys Ala Leu Pro Ile Cys Lys Glu Phe Gly Asn
 140 145 150
 Leu Ser Gln Leu Asn Phe Leu Gly Leu Ser Ala Met Lys Leu Gln
 155 160 165
 Lys Leu Asp Leu Leu Pro Ile Ala His Leu His Leu Ser Tyr Ile
 170 175 180
 Leu Leu Asp Leu Arg Asn Tyr Tyr Ile Lys Glu Asn Glu Thr Glu
 185 190 195
 Ser Leu Gln Ile Leu Asn Ala Lys Thr Leu His Leu Val Phe His
 200 205 210
 Pro Thr Ser Leu Phe Ala Ile Gln Val Asn Ile Ser Val Asn Thr
 215 220 225

Leu	Gly	Cys	Leu	Gln	Leu	Thr	Asn	Ile	Lys	Leu	Asn	Asp	Asp	Asn
				230					235					240
Cys	Gln	Val	Phe	Ile	Lys	Phe	Leu	Ser	Glu	Leu	Thr	Arg	Gly	Pro
				245					250					255
Thr	Leu	Leu	Asn	Phe	Thr	Leu	Asn	His	Ile	Glu	Thr	Thr	Trp	Lys
				260					265					270
Cys	Leu	Val	Arg	Val	Phe	Gln	Phe	Leu	Trp	Pro	Lys	Pro	Val	Glu
				275					280					285
Tyr	Leu	Asn	Ile	Tyr	Asn	Leu	Thr	Ile	Ile	Glu	Ser	Ile	Arg	Glu
				290					295					300
Glu	Asp	Phe	Thr	Tyr	Ser	Lys	Thr	Thr	Leu	Lys	Ala	Leu	Thr	Ile
				305					310					315
Glu	His	Ile	Thr	Asn	Gln	Val	Phe	Leu	Phe	Ser	Gln	Thr	Ala	Leu
				320					325					330
Tyr	Thr	Val	Phe	Ser	Glu	Met	Asn	Ile	Met	Met	Leu	Thr	Ile	Ser
				335					340					345
Asp	Thr	Pro	Phe	Ile	His	Met	Leu	Cys	Pro	His	Ala	Pro	Ser	Thr
				350					355					360
Phe	Lys	Phe	Leu	Asn	Phe	Thr	Gln	Asn	Val	Phe	Thr	Asp	Ser	Ile
				365					370					375
Phe	Glu	Lys	Cys	Ser	Thr	Leu	Val	Lys	Leu	Glu	Thr	Leu	Ile	Leu
				380					385					390
Gln	Lys	Asn	Gly	Leu	Lys	Asp	Leu	Phe	Lys	Val	Gly	Leu	Met	Thr
				395					400					405
Lys	Asp	Met	Pro	Ser	Leu	Glu	Ile	Leu	Asp	Val	Ser	Trp	Asn	Ser
				410					415					420
Leu	Glu	Ser	Gly	Arg	His	Lys	Glu	Asn	Cys	Thr	Trp	Val	Glu	Ser
				425					430					435
Ile	Val	Val	Leu	Asn	Leu	Ser	Ser	Asn	Met	Leu	Thr	Asp	Ser	Val
				440					445					450
Phe	Arg	Cys	Leu	Pro	Pro	Arg	Ile	Lys	Val	Leu	Asp	Leu	His	Ser
				455					460					465
Asn	Lys	Ile	Lys	Ser	Val	Pro	Lys	Gln	Val	Val	Lys	Leu	Glu	Ala
				470					475					480
Leu	Gln	Glu	Leu	Asn	Val	Ala	Phe	Asn	Ser	Leu	Thr	Asp	Leu	Pro
				485					490					495
Gly	Cys	Gly	Ser	Phe	Ser	Ser	Leu	Ser	Val	Leu	Ile	Ile	Asp	His
				500					505					510
Asn	Ser	Val	Ser	His	Pro	Ser	Ala	Asp	Phe	Phe	Gln	Ser	Cys	Gln
				515					520					525
Lys	Met	Arg	Ser	Ile	Lys	Ala	Gly	Asp	Asn	Pro	Phe	Gln	Cys	Thr
				530					535					540
Cys	Glu	Leu	Arg	Glu	Phe	Val	Lys	Asn	Ile	Asp	Gln	Val	Ser	Ser
				545					550					555
Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	Tyr	Lys	Cys	Asp	Tyr	Pro
				560					565					570
Glu	Ser	Tyr	Arg	Gly	Ser	Pro	Leu	Lys	Asp	Phe	His	Met	Ser	Glu
				575					580					585
Leu	Ser	Cys	Asn	Ile	Thr	Leu	Leu	Ile	Val	Thr	Ile	Gly	Ala	Thr
				590					595					600
Met	Leu	Val	Leu	Ala	Val	Thr	Val	Thr	Ser	Leu	Cys	Ile	Tyr	Leu
				605					610					615
Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Val	Cys	Gln	Trp	Thr	Gln	Thr
				620					625					630
Arg	Arg	Arg	Ala	Arg	Asn	Ile	Pro	Leu	Glu	Glu	Leu	Gln	Arg	Asn
				635					640					645
Leu	Gln	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu	His	Asp	Ser	Ala
				650					655					660
Trp	Val	Lys	Ser	Glu	Leu	Val	Pro	Tyr	Leu	Glu	Lys	Glu	Asp	Ile
				665					670					675
Gln	Ile	Cys	Leu	His	Glu	Arg	Asn	Phe	Val	Pro	Gly	Lys	Ser	Ile
				680					685					690
Val	Glu	Asn	Ile	Ile	Asn	Cys	Ile	Glu	Lys	Ser	Tyr	Lys	Ser	Ile
				695					700					705
Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Ser	Glu	Trp	Cys	His	Tyr
				710					715					720
Glu	Leu	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn

				725					730					735
Asn	Leu	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile
				740					745					750
Pro	Asn	Lys	Tyr	His	Lys	Leu	Lys	Ala	Leu	Met	Thr	Gln	Arg	Thr
				755					760					765
Tyr	Leu	Gln	Trp	Pro	Lys	Glu	Lys	Ser	Lys	Arg	Gly	Ala	Leu	Leu
				770					775					780

Gly

<210> 89
 <211> 293
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: LI:236386.4.orf2:2000MAY01

<400> 89

Trp	His	Lys	Ile	Ala	Glu	Thr	Tyr	Ser	Ile	Glu	Met	Gly	Pro	Arg
1				5					10					15
Gly	Pro	Gln	Cys	Glu	Gly	Ala	Ile	Pro	Thr	His	Leu	Pro	Ala	Leu
				20					25					30
Trp	Arg	Thr	Pro	Gln	Asn	Arg	Pro	Asn	Ser	Arg	Ala	Ser	Lys	Ala
				35					40					45
Thr	Ser	Pro	Thr	Ser	Ser	His	Pro	Pro	Met	Leu	Pro	His	Pro	Ser
				50					55					60
Thr	Gly	Ala	Thr	Asn	Thr	Leu	Thr	Gly	Ser	Ile	Thr	Arg	Leu	Leu
				65					70					75
His	Lys	Phe	Thr	Val	Ile	Ser	Val	Pro	His	Leu	Pro	Glu	Lys	Gln
				80					85					90
Ala	Thr	Gly	Arg	Phe	Glu	Glu	Asp	Phe	Ile	Glu	Lys	Arg	Lys	Arg
				95					100					105
Arg	Leu	Ile	Leu	Trp	Met	Asp	His	Met	Thr	Ser	His	Pro	Val	Leu
				110					115					120
Ser	Gln	Tyr	Glu	Gly	Phe	Gln	His	Phe	Leu	Ser	Cys	Leu	Asp	Asp
				125					130					135
Lys	Gln	Trp	Lys	Met	Gly	Lys	Arg	Arg	Ala	Glu	Lys	Asp	Glu	Met
				140					145					150
Val	Gly	Ala	Ser	Phe	Leu	Leu	Thr	Phe	Gln	Ile	Pro	Thr	Glu	His
				155					160					165
Gln	Asp	Leu	Gln	Asp	Val	Glu	Asp	Arg	Val	Asp	Thr	Phe	Lys	Ala
				170					175					180
Phe	Ser	Lys	Lys	Met	Asp	Asp	Ser	Val	Leu	Gln	Leu	Ser	Thr	Val
				185					190					195
Ala	Ser	Glu	Leu	Val	Arg	Lys	His	Val	Gly	Gly	Phe	Pro	Gln	Gly
				200					205					210
Ile	Pro	Glu	Arg	Trp	Ala	Val	Pro	Ser	Arg	Pro	Ser	Val	Ile	Pro
				215					220					225
Ser	Arg	Trp	Thr	Pro	Pro	Phe	Ala	Leu	Arg	Pro	Ser	Thr	Val	Pro
				230					235					240
Phe	Leu	Thr	Arg	Ala	Val	Pro	Met	Lys	Pro	Ser	Gly	Arg	Cys	Leu
				245					250					255
Leu	Ser	Ser	Pro	Arg	Met	Thr	Ser	Ser	Arg	Cys	Trp	Thr	His	Cys
				260					265					270
Leu	Ser	Thr	Arg	Ala	Cys	Ser	Pro	Thr	Ser	Leu	Thr	Ser	Ser	Ile
				275					280					285
Tyr	Lys	Lys	Ala	Pro	Ser	Pro	Arg							
				290										

<210> 90
 <211> 241
 <212> PRT
 <213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: LI:252904.5.orf1:2000MAY01

<400> 90

Thr	Pro	Cys	Leu	Gln	Glu	Val	Ala	Gly	Pro	Leu	Leu	Asp	Gly	Met
1				5					10					15
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala
				20					25					30
Gln	Val	Arg	Val	Tyr	Glu	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu
				35					40					45
Pro	Ser	Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His
				50					55					60
Gly	Asn	Lys	Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro
				65					70					75
Val	Thr	Ala	Phe	Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr
				80					85					90
Arg	His	Pro	Ser	Leu	Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala
				95					100					105
Met	Ala	Glu	Gly	Ser	Val	Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro
				110					115					120
Gly	Pro	His	Asn	Phe	Tyr	Ser	Arg	Pro	His	Phe	Val	Asn	Thr	Val
				125					130					135
Glu	Met	Phe	Asp	Leu	Glu	His	Gly	Ser	Trp	Thr	Lys	Leu	Pro	Arg
				140					145					150
Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala	Asp	Phe	Val	Val	Gly	Ser
				155					160					165
Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly	Leu	Gly	Asn	Gln	Pro
				170					175					180
Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu	Ala	Arg	Arg	Arg
				185					190					195
Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys	Ser	Cys	Ser
				200					205					210
Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly	Val	Ala
				215					220					225
Gln	Gly	Pro	Ser	Gln	Ala	Val	Glu	Ala	Leu	Cys	Leu	Arg	Asp	Gly
				230					235					240
Val														